

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2004, 20:12:36 ; Search time 3601 Seconds  
(without alignments)

5365.407 Million cell updates/sec

Title: US-10-086-464-2  
Perfect score: 3453  
Sequence: 1 MSAPSPGTCGSPSPSNT.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US10086464/runat\_23042004\_083015\_5625/app.query.fasta\_1.839  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOQPC=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10086464 @CGN 1 1 4237 @runat\_23042004\_083015\_5625 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estm:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vri:\*
- 28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1092.5	31.6	1084	12	BP184771
2	1090.5	31.6	824	14	CD435142
3	1086	31.5	788	14	CF436437
4	1071	31.0	789	14	CF436655
5	1069	31.0	759	12	BM408099
6	1066	30.9	785	14	CF436122
7	1065	30.8	757	12	BG596561
8	1063	30.8	731	14	CB655196
9	1047	30.3	692	12	BG441204
10	1030	29.8	723	14	CD839231
11	1027.5	29.8	1053	11	AY108241
12	1025	29.7	1016	11	AY108243
13	1018	29.5	666	12	BM358715
14	1013	29.3	695	13	CA072174
15	983	28.5	715	13	BQ099573
16	961	27.8	770	13	BQ999193
17	931	27.0	611	14	CA237156
18	931	27.0	859	29	CC725849
19	929.5	26.9	809	14	CA765135
20	928	26.9	850	29	CC687554
21	923.5	26.7	769	14	CK283399
22	921	26.7	618	14	CA269355
23	921	26.7	651	14	CF478389
24	920	26.6	673	14	CA164704
25	919.5	26.6	938	29	CG333846
26	917.5	26.6	949	29	CG436431
27	912	26.4	679	13	BQ404121
28	904.5	26.2	674	14	CA298046
29	903	26.2	595	14	CF015663
30	903	26.2	637	13	BQ134241
31	903	26.2	645	13	BQ506869
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33	895.5	25.9	682	13	CA095337
34	895	25.9	641	14	CA248316
35	895	25.9	725	29	CG450877
36	893.5	25.9	803	14	CF243440
37	891	25.8	646	13	BQ240617
38	891	25.8	652	13	BQ496883
39	891	25.8	666	13	BU499754
40	891	25.8	691	14	CA237152
41	889	25.7	626	13	BQ582873
42	888.5	25.7	593	10	BF176907
43	887	25.7	622	14	CA999610
44	887	25.7	673	13	BQ410602
45	886.5	25.7	573	9	AV551753

ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION BP184771 pns rice panicle cDNA, germ cell generating stage Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.  
ACCESSION BP184771  
VERSION BP184771.1  
KEYWORDS GI:32948199  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE
AUTHORS      Moriguchi,K., Ito,Y., Yamazaki,Y. and Kurata,N.
TITLE        Finding of various plant nuclear proteins using yeast nuclear
              transposition trap system - a proteomal approach
JOURNAL      Unpublished (2003)
COMMENT      Contact: Kazuki Moriguchi
              Plant Genetics
              National Institute of Genetics
              Yata 1111, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-55-981-6872
              Fax: 81-55-981-6879
              Email: kmoriguc@lab.nig.ac.jp
              cDNA clone obtained from nuclear transportation trap system
              encoding a protein similar to Oryza sativa (japonica
              cultivar-group) putative receptor protein kinase PERK1.
FEATURES
source      Location/Qualifiers
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            /dev_stage="germ cell generating stage"
            /clone_lib="pNS rice panicle cDNA, germ cell generating
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ORIGIN
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Percent Similarity: 82.88%      Conservative: 30
Best Local Similarity: 72.60%      Mismatches: 43
Query Match:    31.64%      Indels:      7
DB:             12      Gaps:      3

US-10-086-464-2 (1-647) x BP184771 (1-1084)
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DB 2 TTGCACGGAAGGCGGACCAACATGGAGTGCGCCACAGCTAAAGATTGCTTTGGGA 61
QY 380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399
DB 62 GCTGCAAAAGGGTTAGCTTATCTTCATGAAGACTGCCATCTCAAGATCATCATCGTGAT 121
QY 400 IleLysAlaSerAsnIleLeuLysPheLysPheGluAlaLysValAlaAspPheGly 419
DB 122 ATTAAGGCGTCAAAACATCTCTTGATTTAAGTTGAATCTAAGGTGCTGATTTTGA 181
QY 420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
DB 182 CTTGTGAAGTTCCACGAGTGAATAACACTCATGTTTCGACAAGAGTAATGGCACTTTT 241
QY 440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
DB 242 GGATATCTAGCACCAAGAGTACGATCTCTGTCGAAGCTCACTGAGAAATCGATGCTTC 301
QY 460 SerPheGlyValValIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 479
DB 302 TCCATGAGGATTATGCTCTTGAGTTAATACTGGTGGCCAGTTGATACAACATCA 361
QY 480 ValTyrValAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
DB 362 ACATATATGATGACAGCTTGGTTCAGTGGGCAAGGCCCTTTACTGATCAAGCACTTGG 421
QY 500 GlnGlyAspPheGluGlyLeuAlaAlaPheAlaLysMetAsnAsnGlyTyrAspArgGlu 519
DB 422 AATGGTAACACGAGGAGTTAGTAGATCTCTGGCTTGGGAGGATTTCAATCCCAATGAG 481
QY 520 MetAlaArgMetValAlaCysAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 539
DB 482 ATGGGAGAAATGATTGCTTGTCAGCTGATCGGTACGCCATTCGCTCGTGGCCCA 541
QY 540 ArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGlu 559

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DB 542 CGCATGAGCCAGGTGTTCGGGCTTTGCAAGGTGACGTGCTTTGGAGGATCTTAATCAA 601
QY 560 GlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAsp 579
DB 602 GGTGTTGGCCTGTGTCACAGCCGCTATTTTGGATCGTAC---AGCAGCTCTGACTATGAT 658
QY 580 SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGlu 599
DB 659 TCTGGCCNATACACAGGAGCATGAGAGTTTCAGGAGATGGCTTTT---ACCAACAAT 715
QY 600 TyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGly 619
DB 716 AATGATACAGCAGTCAATACAGCGCACCAACACGAGTATGGCCAGATACCCCTCTGCA 775
QY 620 SerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly 639
DB 776 TCAAGCAGCGAGGGCCAAACAAACCCAGGAAGTTCAGGACGAGGACCAACCAAGAGGCGGC 835
QY 640 -----GlnGlyTyrSerGlyProSer 646
DB 836 TACAGTGGCTACAGCTCAGGATACAGCGGAGCCTCA 871

RESULT 2
CD435142
LOCUS      CD435142
DEFINITION EL01N0355D03.b EndospERM_3 Zea mays cDNA, mRNA linear EST 03-JUN-2003
ACCESSION  CD435142
VERSION    CD435142.1 GI:31350785
KEYWORDS  EST.
SOURCE     Zea mays
ORGANISM  Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 824)
AUTHORS   Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
           Messing,J.
TITLE     Sequencing of the maize endospERM ESTs
JOURNAL   Unpublished (2002)
COMMENT   Contact: Lai, Jinsheng
           Dr. Joachim Messing's lab
           Waksman Institute, Rutgers University
           190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
           Tel: 732-445-3801
           Fax: 732-445-5735
           Email: jlai@waksman.rutgers.edu
           Seq primer: T3.
FEATURES  Location/Qualifiers
           source
           1..824
           /organism="Zea mays"
           /mol_type="mRNA"
           /cultivar="W22"
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           /tissue_type="EndospERM of 7-23DAP"
           /clone_lib="EndospERM 3"
           /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
           XhoI"

ORIGIN
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Percent Similarity: 84.12%      Conservative: 27
Best Local Similarity: 74.37%      Mismatches: 41
Query Match:    31.58%      Indels:      3
DB:             14      Gaps:      2

US-10-086-464-2 (1-647) x CD435142 (1-824)
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DB 2 TTGGTTGGCTATTGCATTTCTGGAGGACCTTGCTGCTGTCTATGATGTTTGCCCAAT 61

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Qy 354 AsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArg 373  
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 Db 62 AACACATTGGAATTCACCTTACATCGCAAGGTGCAACAACTATGGAGTGGCTGTGCTAGA 121  
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 Qy 374 LeuLysLeuAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnPro 393  
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 Db 122 TTAAGATCATGTTGGGTGCTGCCAAGGGTTTACCTTATCTTATGAAAGACTGCCATCCA 181  
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 Qy 394 LysLeuLeuHisArgAspLysLeuAlaSerAsnLeuLeuLeuAspPheLysPheGluAla 413  
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 Db 182 AAGATCATCCATCGTGACATAAAGGCATCTAACATTCTTCTGACTTCCAATTGAGCT 241  
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 Qy 414 LysValAlaLeuPheGlyLeuAlaLysLeuAlaSerAspThrAsnThrHisValSerThr 433  
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 Db 242 AAGGTTCTGCTGATTTGGACTTGCACAGTTTCACTACTGATTAACACACCCATGTTTCGACA 301  
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 Db 302 AGAGTAATGGCACCTTTGGGTATTTGGCACCTGAGTATGATCATCTTCTGGCAAGCTAACCA 361  
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 Db 362 GAAATCCGATGATTTCTTCTCGAGTCTATGCTTCTGAGCTTATTAATCTGGGGCGGA 421  
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 Qy 474 ProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspThrAlaArgProLeu 493  
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 Db 422 CCAGTTGCACACACCAACATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481  
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 Qy 494 LeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaLeuAlaLysMetAsnAsn 513  
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 Db 482 CTGATCGGAGCCTTTGGAGTGGTGAATGATGATTTCTTTTGGTGGTCTCTGGGGGGAAG 541  
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 Db 602 TCTGCAGCTCGTCCGCCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661  
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 Db 662 TTGGAGACCTTAATGAAGGTGTTTCGGCTGGCCATAGCCGCTTCTTTGGGTCTATC--- 718  
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 Qy 574 GlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMet 593  
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RESULT 3  
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 LOCUS 788 bp mRNA linear EST 04-SEP-2003  
 DEFINITION EST672782 normalized cDNA library of onion Allium cepa cDNA clone  
 ACACM44, mRNA sequence.  
 ACCESSION CF436437  
 VERSION CF436437.1 GI:34459127  
 KEYWORDS EST.  
 SOURCE Allium cepa (onion)  
 ORGANISM Allium cepa  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 Allium.  
 REFERENCE 1 (bases 1 to 788)  
 AUTHORS Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.  
 TITLE Expressed Sequence Tags from a normalized library of mixed onion  
 tissues (Allium cepa)  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Havey MJ  
 Department of Horticulture

USDA-ARS and University of Wisconsin  
 1575 Linden Drive, Madison, WI 53706, USA  
 Tel: 608-262-1830  
 Fax: 608-262-4743  
 Email: mjhhavey@facstaff.wisc.edu  
 TIGR sequence name ACACM44TR. For more information:  
 http://haveylab.hort.wisc.edu  
 Seq primer: CAG GAA ACA GCT ATG ACC.

## FEATURES

Location/Qualifiers  
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 /organism="Allium cepa"  
 /mol\_type="mRNA"  
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 Texas Legend(roots)"  
 /db\_xref="taxon:4679"  
 /clone="ACACM44"  
 /tissue\_type="Callus, roots, and young bulbs"  
 /clone\_lib="normalized cDNA library of onion"  
 /notes="Vector: pCMVSPORT6.1-ccdb (Invitrogen); Site 1:  
 EcorV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA  
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 synthesize the library. Normalization to enrich for  
 low-copy transcripts was performed by proprietary  
 techniques of Invitrogen."

## ORIGIN

Alignment Scores:  
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 Best Local Similarity: 77.86% Mismatches: 32  
 Query Match: 31.45% Indels: 0  
 DB: 14 Gaps: 0  
 US-10-086-464-2 (1-647) x CF436437 (1-788)

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 Qy 280 LeuLeuGlyGlnGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGlu 299  
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 Qy 320 ValGluLeuLeuSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysAla 339  
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 Qy 340 AlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHis 359  
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US-10-086-464-2 (1-647) x CF436122 (1-785)

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QY 280 LeuLeuGlyGlnGlyPheGlyValHisGlyValLeuProSerGlyLysGlu 299
Db 62 CTTCTTGGCAAGGTGGATTTGGATATGTGCACAAGAGTACTTCCAAACGGTHAAGAA 121
QY 300 ValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGlu 319
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QY 340 AlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnLeuGluLeuHis 359
Db 242 TCAGGAGATCATAGATTTGCTGTATGAATATGTTCTTAATAAAACCCCTTGAGTTCCAT 301
QY 360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379
Db 302 TTGCATGGAAGAAAGATGTTCCACCTATGGATTGGCCACCGGTTAAAAATTCCTTTGGT 361
QY 380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleLeuHisArgAsp 399
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QY 400 IleLysAlaSerAsnIleLeuLysPheGlyValAlaLysValAlaAspPheGly 419
Db 422 ATTAAGCAGCAAAATTTCTTCTGAGATGAATTTGAGGCTAAGTTGCGATTTTGGC 481
QY 420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
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QY 460 SerPheGlyValValLeuLeuLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
Db 602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAAGTTGATGCAACCCAA 661
QY 480 ValTyrValAspAspSer-LeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGly 499
Db 662 ACTTATACAGATGATAGTTTGGTTCGATTTGGCAAGACCAATTCGTCGCAAGGCTATGGA 721
QY 499 uGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGly 519
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QY 519 uMet 520
Db 782 AATG 785
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RESULT 7
BG596561
LOCUS EST495239 cSTS Solanum tuberosum cDNA clone cSTS15A23 5' sequence,
DEFINITION mRNA sequence.
ACCESSION BG596561
VERSION BG596561.1 GI:13614701
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 757)
```

## AUTHORS

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemiango, A.,  
Bougri, O., Buell, C. R., Rinning, C., Tankley, S. and Baker, B.  
Generations of ESTs from sprouting potato eyes  
Unpublished (2000)  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
This clone can be obtained from the University of Arizona Genomics  
Institute. Orders can be made through URL:  
http://genome.arizona.edu/orders/  
Seq primer: M13F-R.

## FEATURES

source

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Location/Qualifiers  
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/mol\_type="mRNA"  
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/db\_xref="taxon:4113"  
/clone="cSTS15A23"  
/tissue\_type="sprouting eyes from tubers"  
/dev\_stage="12-14 weeks post harvest"  
/lab\_host="SOLR"  
/clone\_lib="cSTS"  
/note="Vector: phaluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were  
taken from tubers. The tubers were incubated at 26C in the  
dark for 2-3 weeks prior to sprouting. The eyes were  
frozen in liquid nitrogen immediately upon removal from  
tubers."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,72e-25 Length: 757  
Score: 1065.00 Matches: 200  
Percent Similarity: 89.16% Conservative: 22  
Best Local Similarity: 80.32% Mismatches: 27  
Query Match: 30.84% Indels: 0  
DB: 12 Gaps: 0  
US-10-086-464-2 (1-647) x BG596561 (1-757)

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QY 301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
Db 1 GCAGTTAAACAGCTTAAGCTTGAAGTGCACAAGGGAAACGTGAATTTTCAGCGGAGGTT 60
QY 321 GluIleLeuSerArgValHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
Db 61 GAGATTATAGCCGAGTACATCAAGCATCTTGTCCTCTTGTGGATACCTGCATTACT 120
QY 341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnLeuGluLeuHisLeu 360
Db 121 GGGGCTCAGACACTGCTTGTATTAGTTTGTCTTCCAAACATACTTTGGAATTTTCATTTA 180
QY 361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
Db 181 CACGAAAGGGAAGGCTCTCTTGGATTGGCAATACGGCTAAAGATTGCTCTAGGGTCA 240
QY 381 AlalysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleLeuHisArgAspIle 400
Db 241 GCTAAAGGACTGGCATATCTGCATGAAGACTGCCAACCGAAATCATTCACCGTATATC 300
QY 401 LysAlaSerAsnIleLeuLysAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
Db 301 AAGCAGCATATATATCTATGACTTTAAATTTTGGGGCTAGGTTGCTGATTTTGACTT 360
QY 421 AlalysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
Db 361 GCCAAGCTAACTTCTGATGTTAATATCTATGCTCTCCACGAGTGCATGGAACTTTGGG 420
QY 441 TyrIleAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
Db 421 TATTTGGCTCCAGAAATATGCTTCTCTGAAAGCTTACAGACAAGTCAGACGATATTCCTC 480
```



of the cotton fiber  
Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence stop: 690.  
Location/Qualifiers  
1..692  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ea0012C15f"  
/tissue\_type="Fibers isolated from bolls harvested 7-10 dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Alignment Scores:  
Pred. No.: 9,38e-25 Length: 692  
Score: 1047.00 Matches: 198  
Percent Similarity: 94.71% Conservative: 17  
Best Local Similarity: 87.22% Mismatches: 12  
Query Match: 30.32% Indels: 0  
DB: 12 Gaps: 0

US-10-086-464-2 (1-647) x BG441204 (1-692)

QY 247 LeuProProSerProGlyLeuValLeuGlyPheSerLySerThrPheThrTyrglu 266  
DB 11 CTTCGGCTGGCTACCTGGTATTCTTCGAAAGGACCTTTAGCTATGAA 70  
QY 267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyPhe 286  
DB 71 GAATTAGGAGAGCAACGGATGCTCTCGGAAGTTAACCTCTTGGACAAGGTGTTTT 130  
QY 287 GlyTyrrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306  
DB 131 GGGTACGTACAAAGGAGTTCTCCCTAATGGGAAGGAGTAGCAGTAAGCACTCAAG 190  
QY 307 ValGlySerGlyGlnGlyArgGluPheGlnAlaGluValGluIleIleSerArgVal 326  
DB 191 GCTGGAAGTGGCGAAGCGAGAGAGAAATTCAGGCTGAAGTTGAGATCATTAGCCGCTC 250  
QY 327 HisHisArgHisLeuValSerLeuValGlyTyrrCysIleAlaGlyAlaLysArgLeuLeu 346  
DB 251 CATCAAAACATCTCGTCTCATTTGGTGGGATACTGTATTCTGGGACAAATAAGATGCTT 310  
QY 347 ValTyrrGluPheValProAsnAsnLeuGluHisLeuHisGlyGluGlyArgPro 366  
DB 311 GTTTATGAGTTGTTCCAAACAAACACTTGGAGTTTCACTTGCATGGGAAGGGGCGACTG 370  
QY 367 ThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrr 386  
DB 371 ACCATGGATTGGCCGCAAGGATGAAATTTGCTTTAGGATCTGCAAAAGGAGCTGCATAT 430  
QY 387 LeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeu 406  
DB 431 CTTTCATGAAGATTGTCATCTTAAGATCATTCACCGTGATATTAAAGGCCGCTAATATTCTG 490  
QY 407 IleAspPhePheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAsp 426  
DB 491 TTGGATTTCAAGTTGAACAAAGGTGCTGATTTTGGACTGACGCAAAATGCTTCCGAT 550  
QY 427 ThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrrLeuAlaProGluTyrr 446

DB 551 GTCAACACGACGCTCTCCACCAGGCTGATGGGTACTTTTCGGGTATTAGCCCTGAGTAT 610  
QY 447 AlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeu 466  
DB 611 GCTTCAAGTGGAAAGCTCACTGATAAATCAGATGTTTCTCCTTCGGGGTTCATGCTTTTG 670  
QY 467 GluLeuIleThrGlyArgArg 473  
DB 671 GAGTTGATTACCGGTACAGA 691

RESULT 10  
CD839231  
LOCUS CD839231 723 bp mRNA linear EST 10-JUL-2003  
DEFINITION RFO2.114104F010529 RFO2 Brassica napus cDNA clone RFO2114104, mRNA  
sequence.  
ACCESSION CD839231  
VERSION CD839231.1 GI:32521171  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 723)  
AUTHORS Genoplante,  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
Location/Qualifiers  
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/db\_xref="taxon:3708"  
/clone="RFO2114104"  
/tissue\_type="anthers"  
/clone\_lib="RFO2"

ORIGIN  
Alignment Scores:  
Pred. No.: 3,37e-24 Length: 723  
Score: 1030.00 Matches: 199  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.83% Indels: 0  
DB: 14 Gaps: 0

US-10-086-464-2 (1-647) x CD839231 (1-723)

QY 449 SerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuLeu 468  
DB 2 AGCGAAAGCTCACGGAAGTCTGACGCTTTCTCATTTGGCGTTGCTTTTGAGCTC 61  
QY 469 IleThrGlyArgArgProValAspAlaAsnAsnValTyrrValAspSerLeuValAsp 488  
DB 62 ATTACCGGCGCTCGACCCGTTGATGCCAACAAATGCTATGTAGATGACAGCTTAGTTGAC 121  
QY 489 TrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGlyLeuAlaAsp 508  
DB 122 TGGGCACACCATTTGCTTAACCGAGCATCTGACGAGGAGACTTTTGAGGGTTTACCTGAT 181  
QY 509 AlaLysMetAsnAsnGlyTyrrAspArgGluGluMetAlaArgMetValAlaCysAlaAla 528  
DB 182 GCAAGATGAATAATGGGTATGACAGAGGAGATGGCTCGCATGTTGCTTGCTGCGG 241

Qy 529 AlaCysValArgHisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeu 548  
 Db 242 GCTTGTGTGCGCAATTCAGCTCGCGCAGACCTCGCATGAGCCAGATTGTGCGTGGTTA 301  
 Qy 549 GluGlyAenValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnVal 568  
 Db 302 GAAGGAATGTATCATCTGTGATCTTTAAACGAGGATGAGACCGATCAAGCAATGTA 361  
 Qy 569 TyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLys 588  
 Db 362 TACAGCTCATACGAGGAGCACCAGATTATGACTCGAGCCAGTACATCAATGAACATGAAG 421  
 Qy 589 LysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsn 608  
 Db 422 AAGTTTATAGAAATGGCTCTTTGGAACCTCAAGAGATACAAACGCCACCGGTGAGTACAGTAAT 481  
 Qy 609 ProThrSerAspTyrGlyLeuTyrProSerGlySerSerGluGlyGlnThrThrArg 628  
 Db 482 CCGACGAGCACTATGACTGTACCTCTGTTTCAGACGAGGAGGCGCAACACACACGC 541  
 Qy 629 GluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647  
 Db 542 GAAATGAGATGGGGAAGATTAAAGAACCGGTGAGGTTATAGTGGACCTTCTCTT 598

RESULT 11  
 AY108241 1053 bp mRNA linear HTC 16-OCT-2002  
 LOCUS  
 DEFINITION Zea mays PC0134818 mRNA sequence.  
 ACCESSION AY108241  
 VERSION AY108241.1 GI:21211319  
 KEYWORDS HTC.

ORGANISM  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,  
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
 TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of  
 Overgo Probes

JOURNAL  
 REFERENCE Unpublished (2002)  
 AUTHORS Coe, E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA

COMMENT  
 If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.

FEATURES  
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 1. .1053  
 /organism="Zea mays"  
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 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed DuPont contigs; this resource was  
 assembled by DuPont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

## ORIGIN

Alignment Scores: 5.61e-24 Length: 1053  
 Pred. No.: 1027.50 Matches: 203

Percent Similarity: 79.93% Conservative: 28  
 Best Local Similarity: 70.24% Mismatches: 46  
 Query Match: 29.76% Indels: 12  
 DB: 11 Gaps: 4

US-10-086-464-2 (1-647) x AY108241 (1-1053)

Qy 365 ArgProThrMetGluTyrSerThrArgLeuLysIle-AlaLeuGlySerAlaLysGlyLe 384  
 Db 6 CGTCCG-----GAGTGGCCTGTAGATTAAAGATCATGTTGGGTGCTGCAAGGGTTT 59  
 Qy 384 uSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAs 404  
 Db 60 AGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCATCTCAA 119  
 Qy 404 nIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAl 424  
 Db 120 CATCTCTTCTGACTTCCAAATTGAAGCTAAGTTGCTGATTTGGACTTCGAAAGTTCCAC 179  
 Qy 424 aSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaPr 444  
 Db 180 TACTGATAACAACACCCATGTTTCGACAGAGTAATGGGCACCTTTGGGTATTTGGCACC 239  
 Qy 444 oGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValVa 464  
 Db 240 TGAGTATGCACTTCTGGCAAGCTAAACAGAAAATCCGATGTATTTTCCTTCGGAGTCAT 299  
 Qy 464 lLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnValTyrValAspAs 484  
 Db 300 GCCTCTTGACTTATTACTGCGGGCGGACCACTTACTGATGCGAGCACTTGAGGATGTTGAATGA 359  
 Qy 484 pSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGl 504  
 Db 360 CAGCTTGGTTGACTGGGCAAGGCCATTTACTGATGCGAGCACTTGAGGATGTTGAATGA 419  
 Qy 504 uGlyLeuAlaAspAlaLysMetAsnGlyTyrAspArgGluGluMetAlaArgMetVa 524  
 Db 420 TGCTTTAGTCGATCCTCGGCTGGGAAAGGACTTCAATCTTAATGAGATGCGAAGAATGAT 479  
 Qy 524 lAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgProArgMetSerGlnIl 544  
 Db 480 AGCTGTGCACTGTCATGTCAGCCATTTGCACGTCGTCGCGCACGATGATGATCAGGT 539  
 Qy 544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564  
 Db 540 CGTTCGGGCTTTGGAGGGCAATGTCTTTGGAGGACCTTAATGAAGGTGTTTCGGCCTGG 599  
 Qy 564 yGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAs 584  
 Db 600 CCATAGCCGCTTCTTTGGGTGCATAC---AGCAGCTCCGATTTACGATTTCTGGCCAGTACAA 656  
 Qy 584 nGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGl 604  
 Db 657 CGAGGACATGAAGAGTTCAAGAGATGGCATTCACACACAC-----TATACCAGCAG 710  
 Qy 604 yGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerGluGl 624  
 Db 711 CCAATACAGCGCGCAACACCAAGTGAATATGACAGATACCGTCTGCATCAAGCAGCGAGGG 770  
 Qy 624 yGlnThrArgGluMetGluMetGlyLysIleLysArgThrGly----- 639  
 Db 771 CCACCAAGACCAAGAGATGGAGTGGGTGCAATGAAGAAAGGTGGTACAGTGGTGCTA 830  
 Qy 640 ----GlnGlyTyrSerGlyProSer 646  
 Db 831 CAGCTCAGGATACAGCGAGCCTCG 855

RESULT 12  
 AY108243 1016 bp mRNA linear HTC 16-OCT-2002  
 LOCUS  
 DEFINITION Zea mays PC0134814 mRNA sequence.  
 ACCESSION AY108243  
 VERSION AY108243.1 GI:21211321

**KEYWORDS** HTC.  
**SOURCE** Zea mays  
**ORGANISM** Zea mays  
**REFERENCE** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatoxyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.  
**AUTHORS** 1 (bases 1 to 1016)  
 Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,  
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
**TITLE** Maize Mapping Project/DuPont Consensus Sequences for Design of  
 Overgo Probes  
**JOURNAL** Unpublished (2002)  
**REFERENCE** 2 (bases 1 to 1016)  
**AUTHORS** Coe, E.H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
**COMMENT** If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.  
**FEATURES**  
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 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed Dupont contigs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 6,536-24 Length: 1016  
 Score: 1025.00 Matches: 200  
 Percent Similarity: 82.14% Conservative: 30  
 Best Local Similarity: 71.43% Mismatches: 42  
 Query Match: 29.68% Indels: 8  
 Db: 11 Gaps: 4

US-10-086-464-2 (1-647) x AY108243 (1-1016)  
 QY 373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyLeuHisGluAspCysAsn 392  
 Db 3 AGATTAAAGATCGCTCTGGTGCTGCCAGGGTTAGCTTATCTTCATGAAGACTGCCAT 62  
 QY 393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412  
 Db 63 CCARAGATCATCCACCGGACATTAAGGATCTAACATCTTCTTGACTTCAAAATTTGAA 122  
 QY 413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432  
 Db 123 GCTATGGTTGCTGACTTTGGACTTGCATTTCACTACTACTATAACACACCATCTGTCA 182  
 QY 433 ThrArgValMetGlyThrPheGlyTyLeuAlaProGluTyAlaAlaSerGlyLysLeu 452  
 Db 183 ACAAGAGTATATGGGACCTTTGGGATTTGGCACCGAGATGACAGATCTGGCAAGCTC 242  
 QY 453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuLeuLeuIleThrGlyArg 472  
 Db 243 ACAGAAAAATCGATGATTTCTTTTCGAGTCATGCTCTTTGAGCTTATTACTGGCGG 302  
 QY 473 ArgProValAspAlaAsnValTyValAspAspSerLeuValAspTrpAlaArgPro 492  
 Db 303 CGACCAATTGACACAAACCAACATATATATGATGATGATGATGATGATGATGATGATGAT 362

QY 493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512  
 Db 363 TTACTGATGAGAGCGCTCGAGGATGGTGAATATGATGCTTTGGTGGATCCTCGGCTCGGA 422  
 QY 513 AsnGlyTyAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysValArg 532  
 Db 423 AAGACTTCAATCTTAACAGAGATGCGAAGATGATAGCTCTGGGGCTGCGTGGCTATGCG 482  
 QY 533 HisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGluVal 552  
 Db 483 CATTCGCGACGCTGTCGGCCACGAATGAGTCAGGTCTGCGGCTCTCGAAGGCGACGTG 542  
 QY 553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTySerSerTy 572  
 Db 543 TCTTTGAGGAGACCTTAATGAAGGTGTTCCAGCTGCGCCATAGCCGCTTCTTTGGGTCAAT 602  
 QY 573 GlyGlySerThrAspTyAspSerSerGlnTyAsnGluAspMetLysLysPheArgLys 592  
 Db 603 ---AGCAGCTCTGATTACGATTCGGGCGAGTACACGAGGACATGACAGAGTTCAGGAAG 659  
 QY 593 MetAlaLeuGlyThrGlnGluTyAsnAlaThrGlyGluTySerAsnProThrSerAsp 612  
 Db 660 ACGGCTTCAATAACAACACCTACACGACGAC---CAATACAGCGCGCCCAACAGTGAA 716  
 QY 613 TyrGlyLeuTyProSerGlySerSerGlyGlnTyThrArgGluMet---Glu 631  
 Db 717 TACGGCCAGGTGCGCTCTGGATCAAGCAGCGAGGCGCCGACGAGATGGAGGAG 776  
 QY 632 MetGlyLysIleLysArgThrGly-----GlnGlyTySerGlyProSer 646  
 Db 777 TCGGCTGCAGTGAAGAAAGGTGGCTACAGCGGCTACAGCTCCGGATACAGCGGAGCCTCG 836

BM358715 666 bp mRNA linear EST 09-JAN-2002  
 GA\_Ea0012D16r Gossypium arboreum 7-10 dpa fiber library Gossypium  
 arboreum cDNA clone GA\_Ea0012D16r, mRNA sequence.  
 BM358715  
 BM358715.1 GI:18099461  
 EST.  
 Gossypium arboreum  
 Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatoxyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 666)  
 Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
 Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total High Quality bases = 646  
 Seq primer: TAATACGACTCATATAGGG  
 High quality sequence stop: 666.  
**FEATURES**  
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 /organism="Gossypium arboreum"  
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 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_Ea0012D16r"  
 /tissue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"



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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 7,55e-24 Length: 666
Score: 1018.00 Matches: 191
Percent Similarity: 95.41% Conservative: 17
Best Local Similarity: 87.61% Mismatches: 10
Query Match: 29.48% Indels: 0
DB: 12 Gaps: 0

US-10-086-464-2 (1-647) x EM358715 (1-666)
Qy 247 LeuProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
Db 11 CTTCCGCTCGTCACCTGGTATTTCTTAGTTTCTCGAAAGACACTTTTGTAGTATGAA 70
Qy 267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaLeuLeuGlyGlnGlyPhe 286
Db 71 GAATTAGCGAGACGAGATGGCTTCTCGAAGTTAACTTCTTGACAAAGTGCGTTT 130
Qy 287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
Db 131 GGGTACGTACCAAGAGTTCTCCCTATGGAAGAGTAGCAGTAAGCAACTCAAG 190
Qy 307 ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluLeuLeuSerArgVal 326
Db 191 GCTGGAAGTGGCAAGCGAGAGAGATTTTCAGGCTGAAGTTGAGATCATTTAGCCGCGTC 250
Qy 327 HisHisArgHisLeuValSerLeuValGlyTyrCysLeuAlaGlyAlaLysArgLeuLeu 346
Db 251 CATCACAAACATCTCGTCTCATTTGGTCGATGATTTCTGGGACAAATAAGAAATGCTT 310
Qy 347 ValTyrGluPheValProAsnAsnAsnLeuLeuHisLeuHisGlyGluGlyArgPro 366
Db 311 GTTTATGAGTTTGTTCNAACACACCTTGGAGTTTCATTTGCAATGGAGGGCGACTG 370
Qy 367 ThrMetGluTrpSerThrArgLeuLysLeuAlaLeuGlySerAlaLysGlyLeuSerTyr 386
Db 371 ACCATGATTGGCCGACAGGATGAAATTCCTTTAGGATCTGCAAAAGGACTGGCATAT 430
Qy 387 LeuHisGluAspCysAsnProLysLeuLeuHisArgAspLeuLysAlaSerAsnIleLeu 406
Db 431 CTTTCATGAAGATTCTCATCTTAAGATCATTCACCGTGATATTAAGGCGCTAATATTCG 490
Qy 407 IleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysLeuAlaSerAsp 426
Db 491 TTGGATTTCAGTTTGAAGCAAGGTTGCTGATTTGAGCTAGCGAAATTTGCTTCCGAT 550
Qy 427 ThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyr 446
Db 551 GTCAACAGCGACGCTCCACCAAGGTGATGGTACTTTTCGGGTATTTAGCCCTGAGTAT 610
Qy 447 AlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValVal 464
Db 611 GCCTTCAAGTGAAGACTCACTGATAAATCAGATGTTTCTCTCCGCGGTCAATG 664

RESULT 14
CA072174 695 bp mRNA linear EST 23-SEP-2003
DEFINITION SCCAM1004A11.g AM1 Saccharum officinarum cDNA clone SCCAM1004A11
5', mRNA sequence.
ACCESSION CA072174
VERSION CA072174.1 GI:34924325
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
AUTHORS
```

```

TITLE The libraries that made SUCBST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 004 row: A column: 11
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCAM1004A11"
/lab_host="DH10B"
/clone_lib="AM1"
/notes="Organ: Apical meristem and tissues surrounding of
mature plants; Vector: pSport1; Site_1: SalI; Site_2:
NotI; An unidirectional cDNA library generated from
[Apical meristem and tissues surrounding of mature
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sephatose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucst.lad.ic.unicamp.br/public"

ORIGIN
Alignment Scores:
Pred. No.: 1.13e-23 Length: 695
Score: 1013.00 Matches: 195
Percent Similarity: 91.85% Conservative: 19
Best Local Similarity: 83.69% Mismatches: 16
Query Match: 29.34% Indels: 3
DB: 13 Gaps: 1

US-10-086-464-2 (1-647) x CA072174 (1-695)
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Db 64 AAAGGAGTGTACCAATGTCACAGAGTTGCTTAAAGCAGTTAAGAGATGGAAGTGGC 123
Qy 311 GlnGlyGluArgGluPheGlnAlaGluValCulileleSerArgValHisHisArgHis 330
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Qy 331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
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Qy 351 ValProAsnAsnLeuLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTyr 370
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Db 304 CCGACAAAGACTAAAAATTTGCTGGGTCTGCGAAGGATTTGGCATATCTTCATGAAGAT 363
Qy 391 CysAsnProLysIleLeuHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
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The libraries that made SUCBST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenhariaia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bccccenter.fcav.unesp.br  
Plate: 004 row: A column: 11  
Seq primer: T7 Promoter Primer.  
Location/Qualifiers



Qy 411 PheGluAlaLysAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430  
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 Qy 431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450  
 Db 484 GTTTCACACAGAGTAATGGCAGATTTGGGTACCTAGCACCTGAGTATGCTGCTTCTGGC 543  
 Qy 451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470  
 Db 544 AAGCTCACTGAGAAATCAGATGCTCTCTTTGGAGTAATGCTCTTTGAGCTAATAACT 603  
 Qy 471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490  
 Db 604 GGGCGGCTCT- - - - -GGTAATTCAGACAGGCGAGATGACAACCTTGGGTGACTGGGCA 657  
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RESULT 15  
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 sequence.  
 ACCESSION BU099573  
 VERSION BU099573.1 GI:22547372  
 KEYWORDS Triticum aestivum (bread wheat)  
 SOURCE Triticum aestivum  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Triticeae; Triticum.  
 1 (bases 1 to 715)  
 Anderson, O.D., Chao, S., Close, T.J., Crossman, C., Penton, R.D.,  
 Lazo, G.R., Nguyen H.T., Pham, J., Rausch, C.J., Turuspekov, Y.,  
 Wilson, C., Woo, J. and Zhang, D.  
 The structure and function of the expressed portion of the wheat  
 genomes - Chinese Spring drought stressed root cDNA library  
 Unpublished (2002)  
 Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@pw.usda.gov  
 Sequences have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 Seq primer: SK primer.

FEATURES  
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 normal conditions, then drought stressed to 80%, 70% and  
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 lab). Total RNA was prepared separately for roots  
 collected at the three different drought conditions. Equal  
 amounts of total RNA were pooled from all three samples,  
 poly(A) RNA were purified, one cDNA library was made, and  
 the cDNA clones were in vivo excised to give pBluescript  
 SK(-) phagemids in the TJ Close lab at the University of

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.04e-22 Length: 715  
 Score: 983.00 Matches: 184  
 Percent Similarity: 89.70% Conservative: 25  
 Best Local Similarity: 78.97% Mismatches: 24  
 Query Match: 28.47% Indels: 0  
 DB: 13 Gaps: 0

US-10-086-464-2 (1-647) x BU099573 (1-715)

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 Db 71 GATGGCACAGAGTTGCTGTGAAGCAATTAGACATGGAAGTGGCAGGAGAGCGTGAG 130  
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 Qy 336 GlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 355  
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 Qy 356 LeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLys 375  
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 Db 671 CAAGCACTCGAGGATGGTAATCAGCATGCTTTAGTGGAT 709

Search completed: April 25, 2004, 00:59:49  
 Job time : 3628 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2004, 20:09:36 ; Search time 5876 Seconds  
(without alignments)  
4772.455 Million cell updates/sec

Title: US-10-086-464-2  
Perfect score: 3453  
Sequence: 1 MSSAPSGTGGSPSPSPNST.....REMEMGKIKRTGGQSGPSL 647

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.ats.\*
- 12: gb.ey.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*

- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.in.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	2936.5	85.0	2098	8	AY128792 Arabidops
8	2936.5	85.0	2116	8	AY056788 Arabidops
9	2936.5	85.0	2188	8	AY059901 Arabidops
10	2936.5	85.0	2190	8	AY093065 Arabidops
11	2934.5	85.0	1959	8	BT008409 Arabidops
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35	1480.5	42.9	125021	8	AC007504 Arabidops
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37	1479.5	42.8	125502	8	ATF1L20 Arabidops
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42	1456	42.2	2616	8	AF424623 Arabidops
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ALIGNMENTS

RESULT 1





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RESULT 3  
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ACCESSION AX825705  
VERSION AX825705.1 GI:39751232  
KEYWORDS Brassica napus (rape)  
SOURCE  
ORGANISM  
Goring, D., Silva, N. and Haffani, Y. Z.  
Increasing plant seed production  
Patent: WO 03072763-A 3 04-SEP-2003;  
Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)  
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source  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Db 517 GGAATCGCATCGAGGAGTCTCTCTGTTGTAGTAGTACTCTGATTGTCTCTCTCTCT 576  
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QY	201	ThrProProSerAspHisValValThrSerLeuProProProProProProProPro	220
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## RESULT 5

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ACCESSION	AX825738.1	GI:39751255			
VERSION					
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				



Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1 Goring, D., Silva, N. and Haffani, Y.Z.  
Increasing plant seed production  
Patent: WO 03072763-A 36 04-SEP-2003;  
JOURNAL Goring, Daphne (CA); Silva, Nancy (CA); Haffani, Yosr, Z. (CA)

## FEATURES

source

1. 1959  
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## ORIGIN

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US-10-086-464-2 (1-647) x AX825738 (1-1959)

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 1 (bases 1 to 2098)  
 REFERENCE  
 AUTHORS Tripp M., Southwick A., Karlin-Neumann, G., Nguyen, M., Miranda, M.,  
 Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,  
 Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
 Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,  
 Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,  
 Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-JUL-2002) DNA Sequencing and Technology Center,  
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
 USA  
 COMMENT e-mail for correspondence: arab@sequence.stanford.edu  
 The RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
 Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
 Hayashizaki, Y. and Shinozaki, K.  
 The Salk, Stanford, PGSC (SSP) Consortium members constructed and  
 sequenced the pUNI (ORF) clones using the RAFL cDNAs: Tripp, M.,  
 Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M.,  
 Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R.,  
 Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H.,  
 Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.  
 Tripp, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally  
 to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.  
 (SSP/Stanford) contributed equally to this work as PIs.  
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 1 (bases 1 to 2116)  
 Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayaashizaki,Y., Ihida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Naruseka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Toriumi,M., Theologis,A. and Ecker,J.R.  
 Arabidopsis cDNA clones  
 Unpublished  
 2 (bases 1 to 2116)  
 Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayaashizaki,Y., Ihida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Naruseka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.  
 Direct Submission  
 Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

TITLE  
 JOURNAL RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayaashizaki,Y. and Shinozaki,K.  
 REFERENCE  
 AUTHORS The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

COMMENT  
 Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.  
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 1996. .2116

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ORIGIN

Alignment Scores:  
Pred. No.: 1.33e-63 Length: 2188  
Score: 2936.50 Matches: 574  
Percent Similarity: 90.61% Conservative: 24  
Best Local Similarity: 86.97% Mismatches: 41  
Query Match: 85.04% Indels: 21  
DB: 8 Gaps: 12

US-10-086-464-2 (1-647) x AY059901 (1-2188)

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Db	92	AACTCGAACACCACTCTCTCTCCAGACGCTTCTCTCTCTCCACCACAACTCT 151
Qy	36	SerSerProProPro---ProSerThrIleProThrSerProProSerSerArgSer 54
Db	152	TCTCTCTCTCTCGTCGCGGTCAACTAATTCAACCTCTCTCTCTCTTCTCTCTTTA 211
Qy	55	ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
Db	212	CCT 259
Qy	75	LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
Db	260	CTTCTCTCAACCTTCCCCCTCCGCTCCCATCACTCTCT--TCTCCACGCTCTCCCACACA 316
Qy	95	ProProThr--ArgAnProProProSerValProGlyProProSerAnProSerArg 113
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Qy	152	IleValThrLeuIleCysLeuLeuCysValvalvelvalvalvalvalvalvalvalval 169
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Qy	170	AspAlaTyrtyrValProProProProProGlyProLySalaGlyGlyProtyrGly 189
Db	551	GCTGCTTACTATGTTCT 610
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Qy	268	LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly	287
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Qy	308	GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluLeuLeuLeuSerArgValHis	327
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Qy	348	TyrGluPheValProAsnAsnLeuGluLeuHisLeuHisGlyGluArgProThr	367
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Qy	368	MetGluTrpSerThrArgGluLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu	387
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Qy	408	AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr	427
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Qy	428	AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla	447
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Qy	468	LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal	487
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Qy	488	AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla	507
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Qy	508	AspAlaLysMetAsnAsnGlyTyrAspArgGluMetAlaArgMetValAlaCysAla	527
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

REFERENCE 1 (bases 1 to 1959)  
AUTHORS Cheuk,R., Chen,H., Kim,C.-J., Shinn,P., Bowser,L., Carninci,P.,  
Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,  
Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,  
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,  
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,  
Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,  
Theologis,A. and Ecker,J.R.  
TITLE Arabidopsis ORF clones  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1959)  
AUTHORS Cheuk,R., Chen,H., Kim,C.-J., Shinn,P., Bowser,L., Carninci,P.,  
Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,  
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Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,  
Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,  
Theologis,A. and Ecker,J.R.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory  
(SIGNAL), Plant Biology Laboratory, The Salk Institute for  
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
USA

COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA : "RIKEN  
Arabidopsis Full-length cDNA") : Seki,M., Narusaka,M., Ishida,J.,  
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, POEC (SSP) Consortium members constructed and  
sequenced the PUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,  
Chen,H., Kim,C.-J., Shinn,P., Bowser,L., Chan,M.M., Chang,C.M.,  
Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,  
Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J.,  
Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,  
Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and  
Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to  
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)  
contributed equally to this work as PIs.

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Qy 428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447

Db 1403 AACACTCATGTATCATACCGGTGATGGAACTTTGGGTATTTGGCTCCGGAATATGCT 1462

Qy 448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467

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Db 1703 GCGGCTTGTGTTCGCATTTCAGTCCGCGCAGACCTTCGATGAGGCACATATGACGGGG 1762

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Qy 568 ValTyrSerSerTyrGlyLysSerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587

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Qy 608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGlyGlnThrThr 627

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Qy 628 ArgGluMetGluMetGlyLysIleLysArgThrGlnGlyTyrSerGlyProSerLeu 647

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RESULT 13

LOCUS AY089024 2324 bp mRNA linear PLN 14-APR-2003

DEFINITION Arabidopsis thaliana clone 17909 mRNA, complete sequence.

ACCESSION AY089024

VERSION AY089024.1 GI:21407798

KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 2324)

AUTHORS Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.

TITLE Full-length messenger RNA sequences greatly improve genome annotation

JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)

MEDLINE 22088475

PUBMED 12093376

REFERENCE 2 (bases 1 to 2324)

AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

TITLE Full-length cDNA from Arabidopsis thaliana

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 2324)

AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

TITLE Direct Submission

JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the ws or Llaer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

source

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ORIGIN

Alignment Scores:

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Score: 2885.00 Matches: 570

Percent Similarity: 90.30% Conservative: 26

Best Local Similarity: 86.36% Mismatches: 42

Query Match: 83.55% Indels: 23  
DB: 8 Gaps: 13  
US-10-086-464-2 (1-647) x AY089024 (1-2324)

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Db 333 CTCTCTCAACCT 389

Qy 95 ProProThr---ArgAsnProProProSerValProGlyProProProSerAsnProSerArg 113  
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Qy 114 GluGlySerProArgProProSerSer-----ProSerProProSerProSerSer 131  
Db 447 ---GGATCT 503

Qy 132 AspGlyLeuSerThrGlyValValValGlyValAlaIleGlyGlyValAlaLeuVal 151  
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Qy 152 IleValThrIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 169  
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Db 624 GCT 680

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Qy 408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427  
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Qy 628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647  
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RESULT 14  
AB020746 79706 bp DNA linear PLN 27-DEC-2000  
LOCUS Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24.  
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24.  
ACCESSION AB020746 BAO00014  
VERSION AB020746.1 GI:3985949  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (eices)

Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC and BAC clones

DNA Res. 7 (3), 217-221 (2000)

20363099

10907853

2 (bases 1 to 79706)

Kaneko,T., Katoh,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S. Direct Submission

Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0842, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see [http://www.kazusa.or.jp/kaos/cgi-bin/agd\\_graph.cgi?c=MOB24](http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MOB24)

Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://grmlini.zool.iastate.edu/cgi-bin/sp.cgi>).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.

The 5' clone is MXP5 and the 3' clone is MSD24.

## FEATURES

source

1..79706

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/mol\_type="genomic DNA"

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/db\_xref="taxon:3702"

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/evidence=not experimental

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## CDS

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## CDS

## CDS



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CDS

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**CDS**

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**CDS**

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Percent Similarity:	61.19%	Conservative:	23
Best Local Similarity:	58.83%	Mismatches:	43
Query Match:	75.93%	Indels:	337
DB:	8	Gaps:	19

US-10-086-464-2 (1-647) x AB020746 (1-79706)

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[illegible]

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[illegible]

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Qy	132	AspGlyLeuSerThrGlyValValValGlyLleAlaIleGlyGlyValAlaLeuVal	151
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Qy	152	IleValThrLeuIleCysLeuLeuCysIlsYlsYlsArgAtgArg-----AspGluGlu	169
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Qy	170	AspAlaTyTrValProProProProGlyProLyseAla-----	184
Db	52306	GCTGCTTACTATGTTCTCTCTCTCTCTCCATCTGCTGCCAAAAG-TAAATTCAAAGATCT	52364
Qy	184	-----	184
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Qy	184	-----	184
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Qy	310	GlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArg	329
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Qy	392	-----AsnProIysIleIleHisArgAspIleIysAlaSerAsnIleLeuIleAs	408
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Qy	556	AspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySer	575
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Qy	576	ThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeu	595
Db	54461	ACAGACTATGACACGAGGCAATACAAACGACGACATGATAAAGTTTAGGAAAAATGGCTCTT	54520
Qy	596	GlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeu	615
Db	54521	GGAACTCAAGAAATACCGGCAACCCCGCGAGTACAGTAATCCAACACAGTGACTACGGACTG	54580
Qy	616	TyrProSerGlySerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysile	635
Db	54581	TACCGTCTGGTTCAGCAGTGAAGTCAAGCCACACGAGAAATGGAGATGGGAANGATT	54640
Qy	636	LysArgThrGlyGlnGlyTyrSerGlyProSerLeu	647
Db	54641	AAGAAAACCGGTCAAGGTTATATAGTGGACCTCTCTT	54676
RESULT 15			
AKI03247			
LOCUS	AKI03247	2307 bp mRNA linear PLN 24-JUL-2003	
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone.J033123K23, full insert sequence.		
ACCESSION	AKI03247		
VERSION	AKI03247.1 GI:32988456		
KEYWORDS	FLU_CDNA; CAP trapper.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.		
AUTHORS	The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team., Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group.; Otsomo,Y., Murakami,K., Tida.Y., Sugano,S., Fujimura,T., Suzuki.Y., Tsunoda.Y., Iwaseki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie.Q., Lu,M., Nariawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Ninkura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka.M., Ryu,R., Ueda.M., Matsubara,K., RIKEN., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa.T., Fukuda,S., Hara.A., Hashidume.W., Hayatsu.N., Imotani.K., Ishii.Y., Itoh,M., Kagawa.I., Kondo.S., Konno.H., Miyazaki.A., Osato,N., Ota.Y., Saito,R., Sasaki,D., Saco.K., Shibata,K., Shinsgawa,A., Shiraki,T., Yoshino.M. and Hayashizaki.Y.		
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice		
JOURNAL	Science 301 (5631), 376-379 (2003)		
MEDLINE	22752273		
PUBMED	12869764		
REFERENCE	2 (bases 1 to 2307)		
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,		



Job time : 5988 secs

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Db
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|||||GATTGGCAAGGCCCTTTAATGATGCGAGCATCAGATGATGCAATTTATGATGCTTTAGTG 1647
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Db

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2004, 18:28:17 ; Search time 604 Seconds  
(without alignments)  
4550.636 Million cell updates/sec

Title: US-10-086-464-2

Perfect score: 3453

Sequence: 1 MSAPSPGTCSPSPSPNST.....REMEMGKIKRTGGYSGPSL 647

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3453	100.0	1944	4	AAF77094 Brassica
2	3453	100.0	1944	9	ACF36548 B. napus
3	3453	100.0	2189	9	ACF36549 B. napus
4	2936.5	85.0	1959	9	ACF36557 A. thalia
5	2885	83.6	2324	3	AAC36968 Arabidops
6	1821.5	52.8	1812	9	ACF36554 O. sativa
7	1668	48.3	1515	9	ACF36555 Z. mays P
8	1637.5	47.4	1488	9	ACF36556 G. max PE

9	1507	43.6	2520	4	AAF77096	Aaf77096 Arabidops
10	1504	43.6	2520	9	ACF36551	Acf36551 Arabidops
11	1479.5	42.8	2820	4	AAF77097	Aaf77097 Arabidops
12	1471.5	42.6	2820	9	ACF36552	Acf36552 Arabidops
13	1209.5	35.0	2880	4	AAF77095	Aaf77095 Arabidops
14	1209.5	35.0	2880	9	ACF36550	Acf36550 Arabidops
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17	839.5	24.3	1923	7	ADA70890	Ada70890 Rice gene
18	816.5	23.6	2124	6	ABZ13274	Abz13274 Arabidops
19	804.5	23.3	2865	7	ADA70701	Ada70701 Rice gene
20	802.5	23.2	2011	4	AAH22557	Aah22557 P. patens
21	797	23.1	1730	7	ADA70647	Ada70647 Rice gene
22	793.5	23.0	2823	7	ADA69478	Ada69478 Rice gene
23	782.5	22.7	1419	3	AAC43029	Aac43029 Arabidops
24	782.5	22.7	1419	6	ABZ13121	Abz13121 Arabidops
25	775.5	22.5	1626	3	AAC48313	Aac48313 Arabidops
26	775.5	22.5	1917	7	ADA70527	Ada70527 Rice gene
27	773	22.4	1479	3	AAC43040	Aac43040 Arabidops
28	769.5	22.3	1353	3	AAC42860	Aac42860 Arabidops
29	769.5	22.3	1353	6	ABZ14106	Abz14106 Arabidops
30	766	22.2	1494	3	AAC48560	Aac48560 Arabidops
31	758.5	22.0	1572	3	AAC42898	Aac42898 Arabidops
32	758.5	22.0	1572	6	ABZ13705	Abz13705 Arabidops
33	758.5	22.0	1920	6	AAL45905	Aal45905 A thalian
34	758.5	22.0	2012	3	AAC44847	Aac44847 Arabidops
35	756	21.9	3239	3	AAH79271	Aah79271 Eucalyptu
36	754.5	21.9	2136	7	ADA69829	Ada69829 Rice gene
37	749.5	21.7	1751	3	AAC45313	Aac45313 Arabidops
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39	740.5	21.4	3525	7	ADA71170	Ada71170 Rice gene
40	740	21.4	2868	3	AAH79266	Aah79266 Pinus rad
41	740	21.4	3153	7	ADA71066	Ada71066 Rice gene
42	736.5	21.3	1703	3	AAC46629	Aac46629 Zea mays
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ALIGNMENTS

RESULT 1

AAF77094  
ID AAF77094 standard; DNA; 1944 BP.

XX

XX AAF77094;

XX

DT 17-MAY-2001 (first entry)

XX

DE Brassica napus PERK1 DNA.

XX

KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.

XX

XX Brassica napus.

XX

PN WO200114563-A1.

XX

PD 01-MAR-2001.

XX

PF 18-AUG-2000; 2000WO-CA000966.

XX

PR 19-AUG-1999; 99US-0149466P.

PR 13-OCT-1999; 99US-0159122P.

XX

PA (GORI/) GORING D.

PA (SILV/) SILVA N.

XX

PI Goring D, Silva N;

XX

DR WPI; 2001-244305/25.

XX

PT New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance,

PT

or for producing transgenic plants with increased wounding or pathogen resistance.

Claim 6; Fig 1; 9lpp; English.

The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide function directly

Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 4,628-93 Length: 1944  
Score: 3453.00 Matches: 647  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-086-464-2 (1-647) x AAF77094 (1-1944)

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41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaPro 60  
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QY 241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260  
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QY 261 SerThrPheThrTyrGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280  
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QY 281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300  
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DB 1561 GCTCGCATGTGTCTGTGTCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620  
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QY 601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620



Db 1801 AACCCACGGGTGAGTACAGTAATCCACCAAGTACTATGACCTGTTACCGCTGGTTCA 1860  
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Qy 641 GlyTyrSerGlyProSerLeu 647  
Db 1921 GGTATTAGTGGACCTTCTCTT 1941  
RESULT 2  
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ID ACF36548 standard; cDNA; 1944 BP.  
XX AC ACF36548;  
XX DT 18-DEC-2003 (first entry)  
XX DE B. napus PERK1 receptor kinase encoding cDNA.  
XX KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
XX KW wound; pathogen resistance; plant growth; seed production; gene; ss.  
XX OS Brassica napus:  
XX FH Key Location/Qualifiers  
XX CDS 1. .1944  
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XX PN WO2003072763-A1.  
XX PD 04-SEP-2003.  
XX PF 28-FEB-2003; 2003WO-CA0000274.  
XX PR 28-FEB-2002; 2002CA-02373903.  
XX PR 28-FEB-2002; 2002US-00086464.  
XX PA (GORI/) GORING D.  
XX PA (SILV/) SILVA N.  
XX PA (HAFF/) HAFFANI Y Z.  
XX PI Goring D, Silva N, Haffani YZ;  
XX DR WPI; 2003-712727/67.  
XX DR P-PSDB; ABR82937.  
XX PT Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase  
PT activity.  
XX PS Claim 3; Fig 1A; 123pp; English.  
XX CC The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents a cDNA encoding a B. napus PERK1 receptor kinase  
CC polypeptide  
XX SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Alignment Scores: 4.62e-93 Length: 1944  
Pred. No.: 3453.00 Matches: 647  
Score: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
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Db 61 ACCACCACTCTCTCCAGCTTCGGCTCTCTCCACCAACACCTCTCTCTCTCGCGG 120  
Qy 41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60  
Db 121 CCATCCACTATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
Qy 61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80  
Db 181 CCATCTCCCACTCCATCTACCGGGGATCTCCACCTCTCTCTCTCTCTCTCTCTCTCT 240  
Qy 81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100  
Db 241 CCGCTCCCACTACGCGCGGATCTCCACCGGACCTGTACTCTCTCTCTCTCTCTCTCT 300  
Qy 101 ProProSerValProGlyProProProSerAsnProSerArgGluGlyGlySerProArgPro 120  
Db 301 CCACCTTCAGTCCAGGACCCAGCTCCATCTCTACGGAAGGAGATCTCTCTCGACCT 360  
Qy 121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140  
Db 361 CCATCTCTCTCTCGCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Qy 141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160  
Db 421 GGATCGCCATCGAGGAGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
Qy 161 LysLysLysArgArgAspGluGluAspAlaTyrTyrValProProProProProProPro 180  
Db 481 AAGAAGAAACGACGAGAGACGAAGAAGATGCTTACTATGTCTCTCGCCACCTCTCTCT 540  
Qy 181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnTTPArgGlnGlnAsnAla 200  
Db 541 GGTCCCAAGCCGGAGGACCTTACGGTGGACAGCAACAAATGGCGGCAACAAACGCA 600  
Qy 201 ThrProSerAspHisValValThrSerLeuProProProProProProProProSerPro 220  
Db 601 ACACCCGTCAGATCATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
Qy 221 ProArgGlnProProProProProProPheMetSerSerSerGlyGlySerAsp 240  
Db 661 CCACGGCAACCTCTCTCCACCTCCACCGCTTTCATGAGCAGCAGCGCGGCTCTCGAC 720  
Qy 241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260  
Db 721 TACTCGGACCGTCCAGTCTCTCTCCACCTCTCCAGGGCTGTGTGTGTGTGTGTGTGTGT 780  
Qy 261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280  
Db 781 AGCACTTTCATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGCACTTG 840  
Qy 281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300  
Db 841 TTAGGACAAAGCGGGTTCGGTTACGTGACAAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
Qy 301 AlavLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320

Db 901 GCTGTGAAGCAGCTTGAAAGTTGGAGTGTGTCAGGAGAGAGAGGAGTTCAGGCAGAGGTT 960  
Qy 321 GluIleIleSerArgValIleHisiArgHisLeuValSerLeuValGlyTyrCysIleIlela 340  
Db 961 GAGATCATCAGCAGAGTTCACACAGGAGTCTGGTGTCTCTTGTGGTATTGGCATGCC 1020  
Qy 341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnLeuLeuGluLeuHisLeu 360  
Db 1021 GGTGCCAAAGATTGCTTGTCTATGAGTTGTTCTTAACAACAATCTGAGCTTCACCTC 1080  
Qy 361 HisGlyGluArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380  
Db 1081 CATGGCAGGAGCGGCTTACAATGGAATGAGACACAGATTGAAGATTGCTCTTGGATCT 1140  
Qy 381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400  
Db 1141 GCTAAAGGACTTCTTATCTTCATGAGATTGCAATCTTAAATCAATTCACCGTGATATC 1200  
Qy 401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420  
Db 1201 AAGGCTTCACACATATTGATAGATTCAAGTTTGAAGCTAAGTTGCTGATTTGGTCTT 1260  
Qy 421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440  
Db 1261 GCTAAGATTGCTTCTGTATACAAACACGATGTATCAACACGTTGATGGAACTTTGGG 1320  
Qy 441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460  
Db 1321 TACTTGGCTCCGGAATACGTCACAGCGGAAGCTCACGGAGAAGCTCTGAGCTTTTCTCA 1380  
Qy 461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnVal 480  
Db 1381 TTTGGCGTTGTCTTTGGAGCTCATTTACTGACGTCGACCGTTGATGCCAACAATGTC 1440  
Qy 481 TyrValAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500  
Db 1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTTGCTTAACCGAGCATCTGAGCA 1500  
Qy 501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluMet 520  
Db 1501 GGAGACTTTGAGGGTTTACGTCATCAAGATGAATAATGGGTATGACAGAGGAGATG 1560  
Qy 521 AlaArgMetValAlaCysAlaAlaCysValArgHisSerAlaArgArgProArg 540  
Db 1561 GCTCGATGGTTGCTTGTCTGCGGCTTGTGTTCGCCATTGACCTCGCCGACAGACTCGC 1620  
Qy 541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560  
Db 1621 ATGAGCCAGATTGTGCTGCGTTAGAGGAAATGTATCACTGTCAATCTTAAACGAAGGG 1680  
Qy 561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlySerThrAspTyrAspSer 580  
Db 1681 ATGAGACACAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCATTATGACTCG 1740  
Qy 581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600  
Db 1741 AGCCAGTACATGAGACATGAGAGATTAGGAAATGGCACTTGGAACTCAAGATAC 1800  
Qy 601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620  
Db 1801 AACGCCAGGGTGAGTACAGTAATCCGACCACTGATGGACTGTACCCGCTCGGTTC 1860  
Qy 621 SerSerGluGlyGlnThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640  
Db 1861 AGCAGCGAGGGCCAAACACACCGGAAATGGAGATGGGGAGATTAAAGAAACCGGTGAG 1920  
Qy 641 GlyTyrSerGlyProSerLeu 647  
Db 1921 GGTATAGTGGACCTTCTCTT 1941

RESULT 3

ACF36549

ID ACF36549 standard; cDNA; 2189 BP.

XX ACF36549;  
AC 18-DEC-2003 (first entry)  
DT 18-DEC-2003 (first entry)  
DE B. napus PERK1 receptor kinase encoding cDNA.  
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
KW wound; pathogen resistance; plant growth; seed production; gene; ss.  
OS Brassica napus.  
FH Key Location/Qualifiers  
FT CDS 1..2189  
FT /\*tag= C  
FT /note= "ABR82938; this protein contains the amino acids  
FT corresponding to 5' and 3'UTR regions, though only the  
FT relevant aa residues (ABR82937) is used in the invention"  
FT 5'UTR 1..96  
FT /\*tag= a  
FT CDS 97..2040  
FT /\*tag= b  
FT /transl\_except= (pos: 1332..1334, aa: Phe)  
FT /product= "PERK1"  
FT /note= "ABR82937; proline-rich Extensin-like Receptor  
FT Kinase"  
FT 3'UTR 2041..2189  
FT /\*tag= d  
FT WO2003072763-A1.  
PN 04-SEP-2003.  
PD 28-FEB-2003; 2003WO-CA000274.  
XX 28-FEB-2002; 2002CA-02373903.  
PR 28-FEB-2002; 2002US-00086464.  
XX (GORI/) GORING D.  
PA (SILV/) SILVA N.  
PA (HAFF/) HAFFANI Y Z.  
XX Goring D, Silva N, Haffani YZ;  
XX WPI: 2003-712727/67.  
DR P-FSDB; ABR82937, ABR82938.  
XX Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase  
PT activity.  
XX Disclosure; Fig 1D; 123pp; English.  
XX The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents a cDNA encoding a B. napus PERK1 receptor kinase  
CC polypeptide  
XX Sequence 2189 BP; 544 A; 592 C; 494 G; 559 T; 0 U; 0 Other;  
SQ  
Alignment Scores: 5e-93 Length: 2189  
Pred. No.: 3453.00 Matches: 647  
Score:

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-086-464-2 (1-647) x ACF36549 (1-2189)

Qy 1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20  
Db  
97 ATGTCCTCGGCGCGTCTCGGGGACTGGTTTCGCTCCATCTCCACCAATCAATCCACA 156  
Qy 21 ThrThrThrProProAlaSerAlaProProProThrThrProSerSerProProPro 40  
Db  
157 ACCACCACTCTCTCCAGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 216  
Qy 41 ProSerThrThrProProSerProProSerProProSerProProSerAlaProPro 60  
Db  
217 CCATCCCACTATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276  
Qy 61 ProSerProProThrProSerThrProGlySerProProProProProProProProPro 80  
Db  
277 CCATCTCCCACTCCATCTACGCGCGGATCTCCATCTCTCTCTCTCTCTCTCTCTCTCA 336  
Qy 81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrProPro 100  
Db  
337 CCCCTCCAACTACGCGCGGATCTCCACCGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 396  
Qy 101 ProProSerValProGlyProProProSerProSerProSerProSerProProProPro 120  
Db  
397 CCACCTTCAGTCCAGGACCACTCCCACTCTCTCCGCGGAGGAGATCTCTCTCGACCT 456  
Qy 121 ProSerSerProProProProProProSerProSerProSerProSerProGlyValVal 140  
Db  
457 CCATCT 516  
Qy 141 GlyThrAlaThrGlyValAlaAlaLeuLeuValThrLeuLeuLeuLeuLeuLeuLeu 160  
Db  
517 GGAATCCCATCGGAGGAGTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576  
Qy 161 LysLysLysArgArgArgAspGluGluAspAlaValThrValProProProProProPro 180  
Db  
577 AAGAAGAAACGACGAG 636  
Qy 181 GlyProLysAlaGlyGlyProTyroGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 200  
Db  
637 GGTCCCAAGCGGAGGAGACCTTACGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 696  
Qy 201 ThrProProSerAspHisValValThrSerLeuProProProProProProProProPro 220  
Db  
697 ACACCCCGTCAGATCATGTCTGACGTCATCTACCAACCACTAAGGCTCCATCTCCA 756  
Qy 221 ProArgGlnProProProProProProProProProProPheMetSerSerSerGlySerAsp 240  
Db  
757 CCACGGCAACCTCTCCACCTCCACCGCTTTCATGAGCAGCAGCGGGCTCCGAC 816  
Qy 241 TyrSerAspArgProValLeuProProProProProProProProProProGlyPheSerLys 260  
Db  
817 TACTCGGACCGTCCAGTCTCTCTCTCCACCGTCTCCAGGGCTTGTGTAGGCTCTCCAAA 876  
Qy 261 SerThrPheThrTyroGluLeuAlaArgAlaThrAlaThrAlaThrAlaThrAlaThr 280  
Db  
877 AGCACTTTCAATACGAGGAGCTAGCTAGAGCCCAATGGTTCTCTCGAGGCGAACTTG 936  
Qy 281 LeuGlyGlnGlyGlyPheGlyTyroValHisLysGlyValLeuProProSerGlyLysGluVal 300  
Db  
937 TTAGGACAGCGGGTTCGGTTAGTCTGCACAAAGGTGTGTGTCTAGTGGGAAGAGAGTT 996  
Qy 301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320  
Db  
997 GCTGTGAAGCAGTTGAAAGTTGGAGTGGTTCAGGAGAGAGAGAGAGAGAGAGAGAGAG 1056  
Qy 321 GluThrLeuSerArgValHisHisArgHisLeuValSerLeuValGlyTyroCysIleAla 340

## RESULT 4

ACF36557

ID ACF36557 standard; DNA; 1959 BP.

XX

AC ACF36557;

XX

DT 18-DEC-2003 (first entry)

Qy 641 GlyTyrSerGlyProSerLeu 647

Db

2017 GGTATATAGTGGACCTTCTCTT 2037

1057 GAGATCATCAGCAGAGTTTCCACAGGCATCTGGTGTCTCTTGTGTGTATTGTCATGCC 1116

Qy

341 GlyAlaLysArgLeuLeuValTyroGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360

Db

1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTCTTAACAACAATCTCGAGCTTTCACCTC 1176

Qy

361 HisGlyGluGlyArgProThrMetGluTyrSerThrArgLeuLysIleAlaLeuGlySer 380

Db

1177 CATGGCAGGAGCGGCTTACAATGGATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy

381 AlalysGlyLeuSerTyroLeuHisGluAspCysAsnProLysIleLeuHisArgAspIle 400

Db

1237 GCTAAAGACCTTCTTATCTTCAAGATTGCATCTTAATCTTAATCATCTACCGTATATC 1296

Qy

401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420

Db

1297 AAGCTTTCAACATATTTGATAGATTTCAAGTTTGAAGTTGCTGATTTTGGTCTT 1356

Qy

421 AlalysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440

Db

1357 GCTAAGATTGCTTCTGTATACAAAACACGATGTATCAACACGTTGTATGGGAACCTTTGGG 1416

Qy

441 TyroLeuAlaProGluTyroAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460

Db

1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAGCTCACGGAGAAGTCTGACGTTTCTCA 1476

Qy

461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480

Db

1477 TTTGGCGTGTGCTTTTGGAGCTCATTTACTGGAGCTCGACCGCTTGATGCCAACATGTC 1536

Qy

481 TyrValAspAspSerLeuValAspTyrAlaArgProLeuLeuAsnArgAlaSerGluGln 500

Db

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Qy

501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyroAspArgGluGluMet 520

Db

1597 GGAAGCTTTCAGGGTTAGCTGATGCAAGATGATGATGATGATGATGATGATGATGATG 1656

Qy

521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540

Db

1657 GCTCGCATGCTGT 1716

Qy

541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560

Db

1717 ATGAGCCAGATTGCGTGTGCTTAGAAGGAAATGTATCACTGTGATCTTAAACGAAGGG 1776

Qy

561 MetArgProGlyGlnSerAsnValTyroSerTyroGlyLysSerThrArgProTyroAspSer 580

Db

1777 ATGAGACCGGTCAAGCAATGTATACGCTCATACGAGAGAGACCGATTTATGATCTG 1836

Qy

581 SerGlnTyroAsnGluAspMetLysPheArgLysMetAlaLeuGlyThrGlnGluTyro 600

Db

1837 AGCCAGTACAATGAAGACATGAAGAGTTTATAGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy

601 AsnAlaThrGlyGluTyroSerAsnProThrSerAspTyroGlyLeuTyroProSerGlySer 620

Db

1897 AAGCCACCGGTGAGTACAGTAATCCAGCAGTATGATGATGATGATGATGATGATGATG 1956

Qy

621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640

Db

1957 AGACGAGGAGGCGCAACCAACGCGGAATGGAGATGGGGAAGATTAAGAGAACCGGTGAG 2016

Qy

641 GlyTyrSerGlyProSerLeu 647

Db

2017 GGTATATAGTGGACCTTCTCTT 2037

XX A. thaliana PERK1 protein encoding genomic DNA.  
DE PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
KW wound; pathogen resistance; plant growth; seed production; gene; ds.  
XX Arabidopsis thaliana.  
OS  
XX WO2003072763-A1.  
PN  
XX 04-SEP-2003.  
PD  
XX 28-FEB-2003; 2003WO-CA000274.  
PF  
XX 28-FEB-2002; 2002CA-02373903.  
PR  
XX 28-FEB-2002; 2002US-00086464.  
PR  
XX (GORI/) GORING D.  
PA (SILV/) SILVA N.  
PA (HAF/) HAFANI Y Z.  
PI Goring D, Silva N, Haffani YZ;  
XX WPI; 2003-712727/67.  
DR  
XX Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase  
PT activity.  
XX  
XX Disclosure; Fig 21d; 123pp; English.  
PS  
XX The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents an A. thaliana PERK1 DNA (At3g24550)  
XX  
SQ Sequence 1959 BP; 496 A; 514 C; 425 G; 524 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: Length: 1959  
Score: 2936.50 Matches: 574  
Percent Similarity: 90.61% Conservative: 24  
Best Local Similarity: 85.97% Mismatches: 41  
Query Match: 85.04% Indels: 21  
Dbs: 9 Gaps: 12

US-10-086-464-2 (1-647) x ACF36557 (1-1959)

QY 1 MetSerAlaProSerProGlyThr-----GlySerProProSerProSer 17  
Db 1 ATGTCACAGCGCGTCTCCAGGCACTACTCCATCACCACTCTCCACCGTCTCTCCACA 60  
QY 18 AnSerThrThrThrThrProProAla-----SerAlaProProThrThrPro 35  
Db 61 AACTGCACAACCAACCACTCTCTCCAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 36 SerSerProProPro-----ProSerThrThrThrThrThrThrThrThrThrThr 54  
Db 121 TCTTCT 180  
QY 55 ThrProSerAlaProProProSerProProThrProSerProSerProProPro 74  
Db 181 CCT 228

QY 75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94  
Db 229 CTTCTCAACCTTCCCTCCCTCCATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 285  
QY 95 ProProThr-----ArgAsnProProSerValProGlyProProSerAsnProSerArg 113  
Db 286 CCCTCAAAACCTCGAAGCCCTCCATCTCTCTCAACGAAGACCACCAAAACACTCCCTCA 342  
QY 114 GluGlyGlySerProArgProSerSer-----ProSerProProSerProSer 131  
Db 343 ---GGATCTACTCTAGAACTCCATCAAAACGCTCGCGCTCTGATTTCTTCC 399  
QY 132 AspGlyLeuSerThrGlyValValValValValValValValValValValValVal 151  
Db 400 GATGGATTGCTACCGGAGTTGTTGGTAGAATCGCATTTGAGGAGTGGCTATTCTTGT 459  
QY 152 IleValThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 169  
Db 460 ATACTGACTCTGATTTGTTCTCTGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 519  
QY 170 AspAlaTyrTyrValProProProProProProProProProProProProPro 189  
Db 520 GCTGCTTACTATGTTCT 579  
QY 190 GlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 208  
Db 580 GGTCAACAAACAGTAGTTGGCAACAAACAAACGCGTCACGCGCGTCAGATAATCATGTAGTG 639  
QY 209 ThrSerLeuProProProProProProProProProProProProProProProPro 228  
Db 640 ACGTCATTG---CCACCACTTAAGCCTCCATCTCCACCACCAAAACCTCTCCGCACT 696  
QY 229 ProProPro-----PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247  
Db 697 CCACCACCAAGATTCATGAGTAGCAGTGGTGGTCTGACTATTCGATCTTCGGTCTCT 756  
QY 248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267  
Db 757 CTTCCACCATCTCCAGGCTTGTGTAGGCTTTCTAAAGACACTTTCATTTATGAGGAG 816  
QY 268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlyGlyPheGly 287  
Db 817 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAGAGGGTTTGGT 876  
QY 288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307  
Db 877 TATGTCATAAAGGTATATTGCTAGTGGAAAGAGTTGCTGTGAACAGTTGAAGCT 936  
QY 308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluLeuLeuLeuLeuLeu 327  
Db 937 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTTAGCAGAGTTTCAT 996  
QY 328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347  
Db 997 CACAGGCATTTGGTTTCTCTATTGGTTATTGTATGGCCGGTGTCAAGAGATTACTTGTTC 1056  
QY 348 TyrGluPheValProAsnAsnAsnLeuLeuLeuHisLeuHisGlyGlyGlyArgProThr 367  
Db 1057 TATGATTTGTTTCCAAACAACATCTTCAGTTTCACCTCCATGTTAAGGAGCGGCTACG 1116  
QY 368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387  
Db 1117 ATGGAATGGAGTACTAGATTGAAGATTGCTCTGTGATCTGCTTAAAGAGACTTTTCATATCT 1176  
QY 388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeu 407  
Db 1177 CATGAAGATTGCAATCCGAAATCATTCACCGTGATATTAAAGCGTCAACATATTGATT 1236  
QY 408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427  
Db 1237 GATTTCAATTTGAAGCTAAGTGTGCTGACTTGTGCTTGTCCACAGATTGCTTCTGATACA 1296  
QY 428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447

```
Db      1297 AACACTCATGTATCTACACGGTGATGGGAACCTTTGGGTATTTGGCTCCGGAAATATGCT 1356
Qy      448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
Db      1357 GCAGTGGAAAGCTCACAGAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGAA 1416
Qy      468 LeuIleThrGlyArgArgProValAspAlaAsnValTyrValAspSerLeuVal 487
Db      1417 CTTATTACTGGAGCGCCCTGTTGATGCGAACAATGCTATGTATAGATGACAGCTTAGTT 1476
Qy      488 AspTyrAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
Db      1477 GACTGGCAGCAGCATTTGCTTTAACCGAGCATCTGAGGAAGAGATTTTGAGGGTTTGCT 1536
Qy      508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
Db      1537 GATTCAAAGATGGTAAATGATGATGACAGAGAGAGATGGCTCGCATGTTGCTTGCCT 1596
Qy      528 AlaAlaCysValArgHisSerAlaArgArgProArgMetSerGlnIleValArgAla 547
Db      1597 GCGGCTTGTGTTGCCATTTCAGCTCGCCGACAGACCTCGCATGAGCCAGATAGTACGGGCG 1656
Qy      548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
Db      1657 TTAGAAGGAATGATCGCTGCTGTCTGATCTTAACGAAGGATGAGACCGGGTCAAGCAAC 1716
Qy      568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
Db      1717 GTATACAGCTCATATGGAGGAGACAGACTATGACAGAGCCCAATACACGACGACATG 1776
Qy      588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
Db      1777 ATAAAGTTTAGGAAATGGCTCTTGGAACTCAAGATACGGCACACCGCGCGAGTACAGT 1836
Qy      608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGlyGlnThrThr 627
Db      1837 AATCCAAACAGTGACTAGGACTGTACCCGCTCGTTCAAGCAGTGAAGGTCAAGCCACA 1896
Qy      628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
Db      1897 CGAGAAATGAGATGGGAAGATTAAAGAAACCGGTCAAGTTATAGTGGACCTCTCTT 1956

RESULT 5
AAC36968
ID AAC36968 standard; DNA; 2324 BP.
AC AAC36968;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 15710.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
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XX 23-MAR-1999; 99US-0125788P.
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XX 25-MAR-1999; 99US-0126264P.
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XX 29-MAR-1999; 99US-0126785P.
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XX 01-APR-1999; 99US-0127462P.
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XX 06-APR-1999; 99US-0128234P.
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XX 08-APR-1999; 99US-0128714P.
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XX 16-APR-1999; 99US-0129845P.
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XX 21-MAY-1999; 99US-0135353P.
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XX 24-MAY-1999; 99US-0135629P.
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XX 25-MAY-1999; 99US-0136021P.
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XX 27-MAY-1999; 99US-0136392P.
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XX 01-JUN-1999; 99US-0137222P.
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XX 07-JUN-1999; 99US-0137724P.
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XX 10-JUN-1999; 99US-0138847P.
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XX 14-JUN-1999; 99US-0139119P.
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XX 16-JUN-1999; 99US-0139452P.
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XX 17-JUN-1999; 99US-0139492P.
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XX 18-JUN-1999; 99US-0139454P.
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XX 18-JUN-1999; 99US-0139455P.
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XX 18-JUN-1999; 99US-0139456P.
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XX 18-JUN-1999; 99US-0139461P.
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XX 18-JUN-1999; 99US-0139462P.
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XX 18-JUN-1999; 99US-0139463P.
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XX 18-JUN-1999; 99US-0139750P.
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XX 18-JUN-1999; 99US-0139763P.
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XX 21-JUN-1999; 99US-0139817P.
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XX 22-JUN-1999; 99US-0139899P.
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XX 06-JUL-1999; 99US-0142390P.
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XX 19-JUL-1999; 99US-0144325P.
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XX 19-JUL-1999; 99US-0144331P.
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XX 19-JUL-1999; 99US-0144332P.
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Hybridisation assay; genetic mapping; gene expression control;  
protein identification; signal transduction pathway; metabolic pathway;  
promoter; termination sequence; ss.







CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents an *O. sativa* PERK protein encoding genomic DNA (TIGR  
CC Accession No. TC102111)

Sequence 1812 BP; 409 A; 487 C; 512 G; 404 T; 0 U; 0 Other;

**Alignment Scores:**

Pred. No.:	1.6e-45	Length:	1812
Score:	1921.50	Matches:	370
Percent Similarity:	71.62%	Conservative:	69
Best Local Similarity:	60.36%	Mismatches:	119
Query Match:	52.75%	Indels:	55
DB:	9	Gaps:	15

US-10-086-464-2 (1-647) x ACF36554 (1-1812)

Qy	54 SerThrProSerAlaProProSerProProThrProSerThrProGlySerProPro 73
	:::     :::     :::     :::     :::     :::     :::
Db	4 TCGTCGCCGTCTGCCTCCGGCCGGTAAACAGACG-----GCCACACCGCCT 51

**Qy** 74 ProLeuProGlnProSer-----ProProAlaPThrThrProGlySerProProAla 91  
||| ||| :: |||||| | ||||||  
**Dp** 52 CCGGGTAAACAGACGGCGGCCACTCCGCAGCAACAATCTGTGTCGCCGCCGCG 111

Qy	92	Pro-----ValThrProProThrArgAsnProProSerValProGlyProProSer	109
		: ::::       ::         ::	
Db	112	CGGGCTTTGTCCGCCCTGGTGAGC---CTCCCGAGCGGCATCGCTCGTCG	168

Qy	110	AsnProSerArgGluGlySerProArgProSerSerPro	---SerProProSer	128
Dh	169	ACC	---ACGCTCTCTCCGAGGCGGCGGCGGCGG	201

Qy 129 ProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAla 148

Dh 203 GCTTCAGTCCGGCTGACACGCGCTGCTGCTGCGGAGCGGCGGCGGCTGCTC 261

**Qy**      149 LeuLeuValIleValThr-----LeuIleCysLeuLeuCysLysLysLysArgArgArg  
          :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
**Dh**      263 CMCCTCCCTGCCTGCGTACCAATCCCTTCCTCCCTCCCTCACACAGACAGACGCCACCAC

[illegible][illegible]

Qy 195 TrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuProProPro 214

Qy 215 ProIysAlaProSerProProArgGlnProProProProProPheMetSer 234

Qy 235 SerSerGlyGlySerAspTyrSer-----AspArgProValLeuProProPro 250

Qy 251 SerProGlyValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArg 270

Qy 271 AlathrAsnGlyPheSerGluAlaAsnLeuGlyGlnGlyGlyPheGlyTyrValHis 290

Qy 291 LysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValcIysSerGly 310

311 GlnGlyGluArgGluPheGlnAlaGluValGluIleLeuSerArgValHisArgHis 3300

Db	775	CAGGGAGCGTGAATTTTCAGCGCGAGGTTTGAGATTATCAGCCGGGTACATCAACAGCAT	834
Qy	331	LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe	350
Db	835	CTTTGTAACATTGGTTGTTATTGTCATTTCTCGAGGGAAGAGGTTGCTTGCTATGAGTAT	894
Qy	351	ValProAsnAsnLeuLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTyr	370
Db	895	GTTTCCAAAACACACATTTGGAGCTTCCATTCGATGGGAGAGGCCGACCAACATGGGAATGG	954
Qy	371	SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp	390
Db	955	CCTCAAGATTAGCATTTGCTTTGGTGTCTGCAAGGGATTGGCATATCTTCATGAAGAT	1014
Qy	391	CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuLeuAspPheLys	410
Db	1015	TGCCATCCTTAAGATCATTTACCGTGACATAAAGTCAGCAAAATATTTCTTTGACGCGAGA	1074
Qy	411	PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis	430
Db	1075	TTTGAGGCAAGGTGGCAGATTTCCGACTTGCAAAATTTGACTTCTGATATAAACATCAT	1134
Qy	431	ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaLaSerGly	450
Db	1135	GTTTTCAACAGAGTAATGGGCATATTTGGGTACTTTGCACACAGATGTCGTCTCTGGC	1194
Qy	451	LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr	470
Db	1195	CAGCTAACTAGAGAAATCAGATGCTTTCTTTCCGAGTAAATGCTTCTTGAGCTAAATACT	1254
Qy	471	GlyArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTyrAla	490
Db	1255	GGCGCGCTCTGTGAGATCGAACCAATCACAGATGGATGACAGCTTGGTTGATGGGCA	1314
Qy	491	ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys	510
Db	1315	AGSCCTTTAATGATCGCAGCATCAGATGATGGCAATATATGATGCTTTAGTGGATCCACG	1374
Qy	511	MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCys	530
Db	1375	CTAGGACAGAGTACAAATGTTAACAGAGATGGCAGAGATGATTCGTTGTGCAGCTGCTTGT	1434
Qy	531	ValArgHisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGly	550
Db	1435	GTACGCCATTTCTGCACGCCGACGCCACCGATGAGCCAGGTTGTTGGGCTTTGGGAAGGC	1494
Qy	551	AsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSer	570
Db	1495	GATGTGTCAATGGATGATCTGAACGAAGGTGTTCTGCTCGCCATAGCCCATCTCTGGGA	1554
Qy	571	SerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPhe	590
Db	1555	TCATAC---AACAGCAACGAGTAGACACACGGGCCATTACAACTAGACCTGAAGAAATTC	1611
Qy	591	ArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThr	610
Db	1612	AGGAAGATGGCATTTGGCAGTGGCAATCTA-----GAGAGCAGCCAGCAAAACG	1659
Qy	611	SerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArg-----	628
Db	1660	CAGCCACCGAGTTGCTCCCAATCGATCCGATCAATGGGGGATGGCGTCAAAATACCG	1719
Qy	629	-----GluMetGluMetGlyLysIleLysArgThrGly	639
Db	1720	GAGACGAGATCGAGATGGGAGTTTGAAGAAAGATGGC	1758

RESULT 7

ACF36555

ID ACF36555 standard; DNA; 1515 BP.

XX

AC ACF36555;

XX

## RESULT 7

ACF36555

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99	0.0000
100	0.0000

XX

AC	ACF
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XX

DT 18-DEC-2003 (first entry)  
DE Z. mays PERK protein encoding genomic DNA.  
XX PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
KW wound; pathogen resistance; plant growth; seed production; maize; gene;  
KW ds.  
XX Zea mays.  
OS WO2003072763-A1.  
PN 04-SEP-2003.  
XX 28-FEB-2003; 2003WO-CA000274.  
XX 28-FEB-2002; 2002CA-02373903.  
PR 28-FEB-2002; 2002US-00086464.  
XX (GORI/) GORING D.  
PA (SILV/) SILVA N.  
PA (HAFF/) HAFFANI Y Z.  
XX Goring D, Silva N, Haffani YZ;  
PI WPI; 2003-712727/67.  
XX Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase  
PT activity.  
XX Disclosure; Fig 21b; 123pp; English.  
XX The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents a Z. mays PERK protein encoding genomic DNA (TIGR  
CC Accession No. AY108241)  
XX SQ Sequence 1515 BP; 400 A; 330 C; 381 G; 404 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4.23e-41 Length: 1515  
Score: 1668.00 Matches: 321  
Percent Similarity: 83.87% Conservative: 43  
Best Local Similarity: 73.96% Mismatches: 59  
Query Match: 48.31% Indels: 12  
DB: 9 Gaps: 4

US-10-086-464-2 (1-647) x ACF36555 (1-1515)

Qy 221 ProArgGlnProProProProProPheMetSerSerSer-----GlyGly 238  
Db 26 CCTCCACAGCGCCAGG-CCACCACCACGAGTGTCTAAATAGTAGTGGCGGATCTGGT 84  
Qy 239 SerAspTyrSerAspArgProValLeuProProSerProGlyLeuValLeuGlyPhe 258  
Db 85 TCTAATTAATCTGGCGGCGAGATCTCTACCTCCACATCCCTGGAGCTGTCTTGGCTTC 144  
Qy 259 SerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAla 278  
Db 145 TCGAAGAGCACATTCACCTACAGAGAGCTGTGTGAGGCTACTGATGATTCCTGGATGCT 204  
Qy 279 AsnLeuLeuGlyGlnGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLys 298

Db 205 AATCTCTCTGGACAAGGTGGTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAA 264  
Qy 299 GluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAla 318  
Db 265 GAGATTGCTGTAAACAAATTGAAACTGGGAAGTGGCCAGGAGAGCGTGAGTTCCAGGCT 324  
Qy 319 GluValGluIleLeuSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCys 338  
Db 325 GAGGTTGAGATTATCAGCCGAGTACATCAACAACACCTTGTGCTTCTTGGTTGGCTATTGC 384  
Qy 339 IleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnLeuGluLeu 358  
Db 385 ATTCTCGGAGCAAGAGGCTGTGCTATGAGTTTGTCCCAATAACATTCGAATTC 444  
Qy 359 HisLeuHisGlyGluGlyArgProThrMetGluTyrSerThrArgLeuValLeuAlaLeu 378  
Db 445 CACTTACATCGGAAAGGTCCACCACANTGGAGTGGCTGCTAGATTAAAGATCAGTTTG 504  
Qy 379 GlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArg 398  
Db 505 GGTGCTGCCAAGGTTTAGCTTATCTTCAATGAAGACTGCCATCCAAAGATCATCATCGT 564  
Qy 399 AspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPhe 418  
Db 565 GACATAAAGGCATCTAAACATTTCTTGAAGCTTCAATTTGAAGCTAAGTTGCTGATTTT 624  
Qy 419 GlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThr 438  
Db 625 GGACTCCAAAGTTCACCTACTGATAACACACCANTGTATCGACACAGAGTAATGGGACC 684  
Qy 439 PheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspVal 458  
Db 685 TTTGGGTATTTGGCACCTGAGTATGCATCTCTGGCAAGCTAAACAGAAAAAATCCGATGA 744  
Qy 459 PheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsn 478  
Db 745 TTTTCTCTCGGAGTCATGCTTCTTGAGCTTATTACTGGGCGCGACAGTTGACACAACC 804  
Qy 479 AsnValTyrValAspAspSerLeuValAspTyrAlaArgProLeuLeuAsnArgAlaSer 498  
Db 805 CAACATATATGATGATGACACTTGGTTGACTGGCAAGGCCANTTACTGATCGCGAGCATT 864  
Qy 499 GluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGlu 518  
Db 865 GAGGATCGTCAATATGATGCTTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAAT 924  
Qy 519 GluMetAlaArgMetValAlaCysAlaAlaCysValArgHisSerAlaArgArgArg 538  
Db 925 GAGATGGCAAGAATGATAGCTGTGCAGCTGCATGTGTAGCCCATTTCTGCACGTCGTCGG 984  
Qy 539 ProArgMetSerGlnIleValArgAlaLeuGluGlyValSerLeuSerAspLeuAsn 558  
Db 985 CCACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1044  
Qy 559 GluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyr 578  
Db 1045 GAAGGTGTTTGGGCTTGGCCATAGCCGCTTCTTGGGTTCATAC---AGCAGCTCCGATTAC 1101  
Qy 579 AspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGln 598  
Db 1102 GATTCTGGCCAGTACACACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCACAACAAC 1161  
Qy 599 GluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer 618  
Db 1162 -----TATACCAGCAGCCCAATCAGCGCCCAACAGTAGTGAATATGACAGATACCGTCT 1215  
Qy 619 GlySerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThr 638  
Db 1216 GCATCAGCAGCGAGGCGCCACGAGCCAGAGAGATGAGTGGGTGGGTGCAATGCAAGAAAGT 1275  
Qy 639 Gly-----GlnGlyTyrSerGlyProSer 646

Db 1276 GGCTACAGTGGTGGCTACAGCTCAGGATACAGCGGAGCCTCG 1317

RESULT 8

ACF36556

ID ACF36556 standard; DNA; 1488 BP.

XX ACF36556;

AC ACF36556;

DT 18-DEC-2003 (first entry)

XX

DE G. max PERK partial EST sequence.

XX

KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;

KW wound; pathogen resistance; plant growth; seed production; soybean; gene;

KW ds.

XX Glycine max.

OS

XX WO2003072763-A1.

PN

XX

PD 04-SEP-2003.

XX

XX 28-FEB-2003; 2003WO-CA000274.

PF

XX 28-FEB-2002; 2002CA-02373903.

PR

XX 28-FEB-2002; 2002US-00086464.

PR

XX (GORI/) GORING D.

PA (SILV/) SILVA N.

PA (HAFF/) HAFFANI Y Z.

XX

PI Goring D, Silva N, Haffani YZ;

PI

DR WPI; 2003-712727/67.

DR

XX

PT Producing a transgenic plant having an increased plant resistance, plant

PT growth or seed production comprises transforming a plant with a nucleic

PT acid molecule having a Proline-rich Extensin-like Receptor Kinase

PT activity.

PT

XX Disclosure; Fig 21c; 123pp; English.

PS

XX The invention relates to producing a transgenic plant having increased

CC plant height, number of branches, number of seed pods and/or seed

CC production compared to a non-transgenic plant, and/or quicker flowering

CC or later senescence compared to a non-transgenic plant. The method

CC involves transforming a plant with a vector including a proline-rich

CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic

CC acid molecule having PERK activity. The method, as well as the PERK

CC nucleic acid molecule and polypeptide, are useful in increasing plant

CC resistance to wounding and pathogens and in increasing plant growth and

CC seed production. The nucleic acid molecule and polypeptide may also be

CC used in producing transgenic plants or transgenic host cells. The present

CC sequence represents a G. max PERK EST (expressed sequence tag) partial

CC sequence (TIGR Accession No. TC123698)

XX

SQ Sequence 1488 BP; 412 A; 291 C; 348 G; 437 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3,248-40	Length:	1488
Score:	1637.50	Matches:	312
Percent Similarity:	89.67%	Conservative:	44
Best Local Similarity:	78.59%	Mismatches:	36
Query Match:	47.42%	Indels:	5
Ds:	9	Gaps:	3

US-10-086-464-2 (1-647) x ACF36556 (1-1488)

QY 253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrrGluLeuAlaArgAlaThr 272

Db 3 GGAAATTCATGGGGTCTCTTAAGAGCATTTCAGATGAGAGATTGGCAGCGCCAACT 62

QY 273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyPheGlyTyrrValHisLysGly 292

Db 63 GATGGCTTCTCTGATGCCAACCTCCTTGGACAAGAGGATTGGATATGTGCACAGAGA 122

QY 293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312

Db 123 ATTTCTCCCAACGGCAAGGAGTGGCAGTGAAGCAATTTGAAGGCTGGAAAGCGGCAAGG 182

QY 313 GluArgGluPheGlnAlaGluValGluLeuSerArgValHisHisArgHisLeuVal 332

Db 183 GAGGTGAATTCGAAGCTGAAGATTGAGATAATTAGCGGTGCCATCAACGATCTTGTT 242

QY 333 SerLeuValGlyTyrrCysIleAlaGlyAlaLysArgLeuLeuValTyrrGluPheValPro 352

Db 243 TCTTTGGTTGATACATCATCTGGGTCCAGAGGCTGCTGTTTATGAATTTGTTCC 302

QY 353 AsnAsnLeuLeuGluLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372

Db 303 AACAAACATTTGGAATTCATTTGCATGGAAGAGGAGACCTACCATGGATGGCCACA 362

QY 373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrrLeuHisGluAspCysAsn 392

Db 363 AGACTAGAATTGCTTTAGGATCTGCTAAGGAGACTGGCGTATCTTCATGAAGATTGTCA 422

QY 393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412

Db 423 CCTAAGATCATCATCGTGATATCAAGCTGCCAATCTCTCTGGATTTTAAAGTTTCAA 482

QY 413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432

Db 483 GCAAAGGTTGCAGATTTTCGGTCTTGCAAAAGTTTCTCTGATGCAATACCATGTTTCT 542

QY 433 ThrArgValMetGlyThrPheGlyTyrrLeuAlaProGluTyrrAlaAlaSerGlyLysLeu 452

Db 543 ACTCGAGTGATGGGACTTTTGGGTATTTGGCTCCAGAAATATGCTTCTAGTGGAAAAC 602

QY 453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472

Db 603 ACAGACAAATCAGATGTTTCTCTCAGGAGTCATGCTCTCGAGTTAATAACCGGAGCA 662

QY 473 ArgProValAspAlaAsnAsnValTyrrValAspSerLeuValAspTrpAlaArgPro 492

Db 663 CGGCGCGTCGATAAAAAATCAAACTTTCATGAGGATAGTTTGGTAGACTGGGCTAGGC 722

QY 493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGlyGlyLeuAlaAspAlaLysMetAsn 512

Db 723 TTGCTCACACGAGCTTTGGNAGAGGATGATTTGATTTCTATTATTGACCAAGGCTCCAG 782

QY 513 AsnGlyTyrrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysValArg 532

Db 783 AATGACTATGATCTTAATGAGATGGCAGAAATGGTGGCTTCTGCTGCGGCTTGCAATCG 842

QY 533 HisSerAlaArgArgProArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552

Db 843 CATTCGGCAAGAGTCGACCAAGGATGAGCCAGGTTGTCGCGCTCTCGAAGGAGATGTC 902

QY 553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrrSerSerTy 572

Db 903 TCTCTAGCAGATCTGAATGAAGGAATAGACTGGACACAGCACTATGATATGTTCTCAT 962

QY 573 GlyGlySerThrAspTyrrAspSerSerGlnTyrrAsnGluAspMetLysLysPheArgLys 592

Db 963 --GAAAGCTCAGATTATGACACTGCACAGTACAAGGAAGACATGAAAAGTTTCAGGAAA 1019

QY 593 MetAlaLeuGlyThrGlnGluTyrrAsnAlaThrGlyGluTyrrSerAsnProThrSerAsp 612

Db 1020 ATGGCATTTGGGAACCTCAGGAGTATGGTCAAGAGTACAGTGCCGCTACAAAGTGAG 1079

QY 613 TyrGlyLeuTyrrProSerGlySerSerSerGluGly-----GlnThrThrArgGlu 629

Db 1080 TATGGTTTAACCCCATCAGGCTCAAGTAGTCAAGCACAGAGCCGCCCAACCCACAGGAA 1139

QY 630 MetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrrSerGlyProSer 646

Dbb 1140 ATGGAATGAGAAAGATGAG---AACAACTCAAGGTTTTCAGTGGAAGTTCT 1187

RESULT 9  
AAF77096

ID AAF77096 standard; DNA; 2520 BP.

XX  
AC AAF77096;

XX  
DT 17-MAY-2001 (first entry)

XX  
DE Arabidopsis gene #2.

XX  
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.

XX  
OS Arabidopsis thaliana.

XX  
PN W0200114563-A1.

XX  
PD 01-MAR-2001.

XX  
PF 18-AUG-2000; 2000WO-CA000965.

XX  
PR 19-AUG-1999; 99US-0149466P.

XX  
PX 13-OCT-1999; 99US-0159122P.

XX  
(GORI/) GORING D.  
(SILV/) SILVA N.

PI Goring D, Silva N;  
XX  
XX WPI; 2001-244305/25.

XX  
PT New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance,  
PT or for producing transgenic plants with increased wounding or pathogen resistance.  
XX  
XX Example; Fig 12; 91pp; English.

XX  
CC The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide function directly

XX  
SQ Sequence 2520 BP; 717 A; 553 C; 537 G; 713 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,93e-36 Length: 2520  
Score: 1507.00 Matches: 368  
Percent Similarity: 53.47% Conservatives: 79  
Best Local Similarity: 44.02% Mismatches: 146  
Query Match: 43.64% Indels: 244  
DB: Gaps: 22

US-10-086-464-2 (1-647) x AAF77096 (1-2520)

Qy 3 SerAlaProSerProGlyThrGlySerProProSerProProSerProAanSerThrThr 22  
||||| :|||  
Db 36 TCCTGTCTCTCCAACAACCTCCACTCTTCTCATCTCCACCGTCTAATACCAATTCAACC 95  
Qy 23 ThrProProProAlaSerAlaProProProThrThrProProSerProProProSer 42  
||||| :|||  
Db 96 ACCTCTTCTCCG-----CCGGCTCCGTCCTCTCTCTCTCCTCACTCTCTCAAGGA 146  
Qy 43 ThrIleProThrSerProProSerSerArgSerThrProSerAlaProProProSer 62  
:||| :|||  
Db 147 GACTCATCATCATGCCACTCTCTGATTCACACATCTCCACAGCTCCACAGCTCTTAAC 206  
Qy 63 GACTProThrProSerThrProGlySerProProLeuProGlnProProProProAla 82  
||||| :|||

207 CTCCTCTAAT---TCCTCTAATAACTCTCTCTCCCTCCGTCACAGGCGGTGGAGGAA 263  
 83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProPro 102  
 264 AGAGGAAATGGAGAAACAATGGTGGCAATGATATCCACCGTCACGCGCTCTCTCTCT 323  
 103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg-----Pro 120  
 324 TCT-----CCTCTCTTAGAGTAATGAGAGTAATGCTGGTACGACAGATCATCGCCA 374  
 121 ProSer-----SerProSerProProSerPro-----SerSerAsp 132  
 375 CCAGGAGACACTGGAGGCTCTCCTCAGACACACCTCTCTTCTAGCGAGGAACGAGTGG 434  
 133 Gly-----LeuSerThrGlyValValValValGlyIleAlaIleGly 145  
 435 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGATTAGTCGGA 494  
 146 GlyValAlaLeuLeuValIleValThrLeuLeuCysLeuLeuLeuValLysLysArgArg 165  
 495 GCTGGCACTTTGATGATCGTTCTATTATTGTGTCTTAGACGCCAAAAAGAGAGAAAA 554  
 166 ArgAspGluGluAspAlaTyrValProProProProProGlyProLysAla--- 184  
 555 -----GACTCTCTCTAC-----CCTGAACCCATGAAGATAAAACATATAC 596  
 185 -----GlyGlyPro 187  
 597 ACACCTCTATGTTTCAACAAATAAGAAGCTTAGATTCTTTTATATAAAATTTTCAGGAACCA 656  
 188 TyrGlyGlnGlnGlnThrPargGlnGlnAsnAlaThrProProSerAspHisVal 207  
 657 ATATCAATATATGGAACCAACCAACCAACAATGCTTTCACAGAAATATATCCGAA----- 710  
 208 ValThrSerLeuProProProProLysAlaProSerProPro----- 221  
 711 -----TTGGCACCATAATTACAGGCCCAAAACCAACATCTACTCGTGGTGGGG 761  
 222 ArgGln-ProProProProProPheMetSerSerSerGly-----Glyse 239  
 762 AGCGGTGGACCATACCGGCTCTCTCTCGCGGATGCTTACAAGCGGAGAGATTCTTC 821  
 239 rAspTyrSer-----AspArgProValLeuProProProSerProGlyLeuValLeu 257  
 822 CATGTACTAGGCCCATACGCCAGTTTACCTCTCTCTCGCTCTCTAGCGCTCGG 881  
 257 yPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerG 277  
 882 ATTCACAAAGACACTTTTACTTACCAGAGCTTGGCGGTGCCAACAGGAGGTTTACGGA 941  
 277 uAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerG 297  
 942 TGCTAACCTTTGGACAGGAGGATTTGGGTATGTCCATAAAGGAGCTCTTGCTAGCGG 1001  
 297 YLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheG 317  
 1002 GAAAGAAGTAGCAGTTAAGAGTTTAAAGCGGGGTAGCGGCAAGAGGAGGAGGAGTTTCA 1061  
 317 nAlaGluValGluIleLeuSerArgValHisArgHisLeuValSerLeuValGlyTyr 337  
 1062 AGCTGAGGTCGATCATATTAGCGGTGTCATCATCGGTATCTTGTGTTCTTGGTTGGATA 1121  
 337 rCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnLeuGlu 357  
 1122 TTGCATAGCTGATGGACAGAGGATGTGGTTTATGAGTTTGTCTTAAACAAACTTTGGA 1181  
 357 uLeuHisLeuHisGly----- 362  
 1182 ATATCATCTTTCATGGTTAGACCACCTTAAAAAATTGTAGTACTAAGTTTATTTTCTCTAAT 1241  
 363 -----Glu-GlyArgProThrM 368  
 1242 CTATATATCAAGAAAGTTGTAACCTTAATTTGTTGTGTAGGGAATAAATCTCTCCGGTAA 1301

```
QY 368 etGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuH 388
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1302 TGAAGTCTCCACTAGGTTGCGTATCGCTTAGGTGCTGCGAAGAGACTCGCTTACCTTC 1361
QY 388 taGluAspCys----- 391
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1362 ACGAAGACTGTAAGTTTAAACATTCAACCATCTCATTTTCTTAACCAAGTTGCATAAAAC 1421
QY 392 -----Asn 392
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1422 AGAGAAAGCTCTCTCTGACTAGTGTATTATCTTTTGGCTGAGAAAATGGTGACGCCAT 1481
QY 393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1482 CCTCGATCATTCACCGGACATCAAGCTGCAAAATATCTCTGAGACTTCACTTGTAT 1541
QY 413 Ala----- 413
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1542 GCTATGGTGATAAACTAGTAGTCTGCATTCTCATCTACGGTTTTTCTTAAGACTACATTGA 1601
QY 414 -----LysValAlaAspPheGlyLeuAlaLysIleAlaSerAs 426
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1602 TGACATTTTGCATTTGTTTATTTCAGGTGCGCTGATTGTGGATTAGTAAATTAACATCTGA 1661
QY 426 pThrAsnThrHisValSerThrArgValMetGlyThrPhe-Gly----- 440
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1662 TAAACACACTCATGTATCTACTCTGTGTGATGGAACTTTCGGGTAAAGCGTTTACCGTAT 1721
QY 440 ----- 440
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1722 GATAAGATTGTTGCTGACACTCAAGAAACATAAACCCTTTGTAGACTAACTACTTGTCTTC 1781
QY 441 -----TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrG 454
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1782 TTTCCACAACATGTTAGATATCTAGCTCCAGATATGCTTCAAGCGGTAAATTAACCG 1841
QY 454 LuLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgP 474
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1842 AGAATCCGATGTTTCTCTTACGGAGTTATGTTATGGAACTTATTAACCTGGAACCGAC 1901
QY 474 roValAspAlaAsnValThrValAspSerLeuValAspTrp----- 489
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1902 CGGTTGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGTATTTCATGCATG 1958
QY 489 ----- 489
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1959 TAACTATGATCGGTATATATGTTTTTTCGCCCTTTTTCGGCTACTAATGATCATGAATA 2018
QY 490 ---AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2019 CAGGCTCGCCCTTATGCTCGCGCTAGAGATGGAACTTTAATGAGCTCGCAGAT 2078
QY 509 AlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAla 528
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2079 GCGAGCTTGAAGGCAACTACAAACCGCAAGAAATGGCTCGAATGGTACTTGTGCCGT 2138
QY 529 AlaCysValArgHisSerAlaArgArgProArgMetSer----- 542
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2139 GCTAGCATTCGATTCCTCGGGCGGTAACCGTCAAAAGATGAG-CCAGGTGAATCAAAATTA 2197
QY 543 -----GlnIleVal 545
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2198 TAACTAAAAGTCTATTTTGTGAGAGATAACAAACAAATGTTGTGTTTTCAGATAGTA 2257
QY 546 ArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGln 565
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2258 AGAGCGTTAAGAGGAGAAAGTGTCTTAGATGCTTTAAACGAAGGTGTGAAGCCAGGACAC 2317
QY 566 SerAsnValTyrSerSerTyrGlySerThrAspTyrAspSerSerGlnTyrAsnGlu 585
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2318 AGTAAAGTTTTCGGGTTCATTGGGAGCAAGCTCGGATTATAGTCAGACACATCTTACATGCA 2377
```

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QY 586 AspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr-----AsnAla 602
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2378 GACATGAAGAAATTCAGACAGATAGCTTTTGTGAGCCAAAGAAATCCCAAGTCAGTGACTGT 2437
QY 603 ThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2438 GAAGGAACATCTAGTATGATTCTAGAGATATGGGA 2473

RESULT 10
ACF36551
ID ACF36551 standard; DNA; 2520 BP.
XX
AC ACF36551;
XX
DT 18-DEC-2003 (first entry)
XX
DE Arabidopsis PERK1 receptor related protein encoding DNA.
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
XX (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
WPI; 2003-712727/67.
DR P-PSDB; ABR82940.
XX
XX Producing a transgenic plant having an increased plant resistance, plant
XX growth or seed production comprises transforming a plant with a nucleic
XX acid molecule having a proline-rich Extensin-like Receptor Kinase
XX activity.
XX
XX Disclosure; Fig 12; 123pp; English.
XX
XX The invention relates to producing a transgenic plant having increased
XX plant height, number of branches, number of seed pods and/or seed
XX production compared to a non-transgenic plant, and/or quicker flowering
XX or later senescence compared to a non-transgenic plant. The method
XX involves transforming a plant with a vector including a proline-rich
XX Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
XX acid molecule having PERK activity. The method, as well as the PERK
XX nucleic acid molecule and polypeptide, are useful in increasing plant
XX resistance to wounding and pathogens and in increasing plant growth and
XX seed production. The nucleic acid molecule and polypeptide may also be
XX used in producing transgenic plants or transgenic host cells. The present
XX sequence represents a PERK1 polypeptide related protein encoding genomic
XX DNA from A. thaliana (Accession NO. AAD15491)
SQ Sequence 2520 BP; 717 A; 552 C; 538 G; 713 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.: 3.58e-36 Length: 2520
Score: 1504.00 Matches: 367
Percent Similarity: 53.47% Conservative: 80
Best Local Similarity: 43.90% Mismatches: 146
Query Match: 43.56% Indels: 244
DB: 9 Gaps: 22
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US-10-086-464-2 (1-647) x ACF36551 (1-2520)



Qy	317	nAlaGluValGluLeuIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTy	337
Db	1062	AGCTGAGGTCGATCATATTAGCCGCTGTCATCATCGGTATCTTGTCTTTTGGTGGATA	1121
Qy	337	rCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnLeuGlu	357
Db	1122	TTGCATAGCTGATGGCAGAGGATGTGGTTATAGATTGTTCTTAACAAAACTTTGGA	1181
Qy	357	uLeuHisLeuHisGly	362
Db	1182	ATATCATCTTCATGGTTAGACCACCTTAAAAAACTTTGAGTACTAAGTTTATTTCTCTAAT	1241
Qy	363	-----	368
Db	1242	CTATATATTCAAGAAAGTTGTAACTTAATTTGTGTGTGAGGAGAAAAATCTTTCCGGTAA	1301
Qy	368	etGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrluH	388
Db	1302	TGGAGTCTCCACTAGGTTCGGTATGCCCTTAGTGTCTGCGAAAGNACTCGCTTACCTTC	1361
Qy	388	isGluAspCys	391
Db	1362	ACGAAGACTGTAAAGTTTAAACATTCACCAATTCATCTCTCAATTTCTTAACCAAGTTGCATAAAAC	1421
Qy	392	-----	392
Db	1422	AGAAAAAGCTCTCTCTGACTAGTGTATCTTTTGGCTGAGAAAAATGTCGAGGCCAT	1481
Qy	393	ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu	412
Db	1482	CCTCGGATCAATCACCGGCACATCAAGCTGCAAAATATCTCTTGGACTTCAACTTTGAT	1541
Qy	413	Ala	413
Db	1542	GCTATGCGTATAAATAGTAGTTCATCTACGGTTTTTTGTTTAAGACTACATTGA	1601
Qy	414	-----LysValAlaAspPheGlyLeuAlaLysIleAlaSerAs	426
Db	1602	TGCAATTTTGCAATTTGTTTATTTCAGGTGGCTGATTTTGGATTAGCTAAGTTAAACATCTGA	1661
Qy	426	pThrAsnThrHisValSerThrArgValMetGlyThrPhe-Gly	440
Db	1662	TAAACAACATCATGTATCTACTCGTGTGTGGGAACCTTTCGGGTAAAGCGTTTACCGTAT	1721
Qy	440	-----	440
Db	1722	GATAAGATTGTTTCGTGACACTCAAGAAACATAACCTTTGTAGACTAATCTACTTTGCTTC	1781
Qy	441	-----TyrLeuAlaProGluTyrrAlaAlaSerGlyLysLeuThrG	454
Db	1782	TTTCCACAAACATGTGTAGATATCTAGCTCCAGATATGCTTCAAGCGGTAAATTAACCG	1841
Qy	454	lulysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgp	474
Db	1842	AGAAATCCGATGTTTCTCTACCGAGTATGTTATTGGAACTTATAACTTGGAAAAACGC	1901
Qy	474	roValAspAlaAsnAsnValTyrrValAspAspSerLeuValAspTrp	489
Db	1902	CGGTTGAT---AATAGCATCACCATGGACGACACTTTAGTAGATTGGTATTTCATGCATG	1958
Qy	489	-----	489
Db	1959	TAACATATGATCGTGTATATATGTTTTTCGCCCTTTTTTCGGGTACTAAATGATCATGAATA	2018
Qy	490	---AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp	508
Db	2019	CAGGCTCGGCCTCTTATGGCTCGCGCGCTAGAGATGGAACACTTTAATGAGCTCGCAGAT	2078
Qy	509	AlaLysMetAsnAsnGlyTyrrAspArgGluGluMetAlaArgMetValAlaCysAlaA	528
Db	2079	GCAGGCTTGAAGGCAACTACAAACCCCGCAAGAATGGCTCGAATGGTGACTTTGTGCCGCT	2138
Qy	529	AlaCysValArqHisSerAlaArgArgArgProArgMetSer	542

```

Db 2139 GCTAGCATTCGTCATTCGGGGCGTAACGCTCAAGATGAG-CCAGGTGAATCAAAATTA 2197
Qy 543 -----GlnIleVal 545
Db 2198 TAACTAAAAGTCTATTTTGTGCAGAGATAACAACAAATGTTGGTGTTCAGATAGTA 2257
Qy 546 AtgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGln 565
Db 2258 AGAGGGTTAGAGAGGAGAGTGCCTTAGATGCTTTAAACGAAGGTGTGAAGCCAGGACAC 2317
Qy 566 SerAsnValTyrSerSerTyrGlySerThrAspTyrAspSerSerGlnTyrAsnGlu 585
Db 2318 AGTAAAGTTTACGGGTCAATGGGAGCAAGCTCGGATTATAGTCAGACATCTTACAATGCA 2377
Qy 586 AspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr-----AsnAla 602
Db 2378 GACATGAAGAAATTCAGACAGATAGCTTTGTGCGACCAAGAAATCCCAATCAGTCACTGT 2437
Qy 603 ThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
Db 2438 GAAGGACATCTAGTATGATCTAGAGATATGGGA 2473

RESULT 11
AAF77097
ID AAF77097 standard; DNA; 2820 BP.
XX
AC AAF77097;
XX
DT 17-MAY-2001 (first entry)
XX
DE Arabidopsis gene #3.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI//) GORING D.
PA (SILV//) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,
PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Example; Fig 13; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 2820 BP; 819 A; 629 C; 577 G; 795 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2e-35 Length: 2820
Score: 1479.50 Matches: 367
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Percent Similarity: 50.00% Conservative: 99
Best Local Similarity: 39.38% Mismatches: 151
Query Match: 42.85% Indels: 318
DB: 4 Gaps: 28

US-10-086-464-2 (1-647) x AAF77097 (1-2820)

Qy 1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
Db 52 GTGATTCATCTCTGCTCCCTGAAACC---TCAATGGGACACACCGCTCAACCGGAACA 108
Qy 21 ThrThrThrProProAlaSerAlaProProThrThrThrProSerSerProProPro 40
Db 109 TCG-----CCGTCTAATGAGTCATGCGCGCCACACACCTTCTTCCACCCACCA 159
Qy 41 ProSerThrIleProThrSerProProSerSerSerArgSerThrProSerAlaProPro 60
Db 160 TCATCA-----ATATCTGCTCTCCCGCAGATATCTCCGTTCTTTTACCGCGG 210
Qy 61 ProSerProProThr-----ProSerThrProGlySerProProProLeu 75
Db 211 CTGACACCCACGCAAGAAACGTCACCTCTACATCTCCGTCCTCATCGCGCTGT 270
Qy 76 -----ProGln-----ProSerProProAlaPro-----Thr 84
Db 271 GTAGCTAATCGCTCAGCGAGACTCCAGAGAATCTTCTCCACCTGCACCTGAAGGCTCA 330
Qy 85 ThrProGlySerProProAla---ProValThrPro-----ProThrArgAsn 99
Db 331 ACTCTGTAAACGACCTGCAACCAACACCGTCGAACCAATATCCCGGAAAGACCA 390
Qy 100 ProProPro-----ProGln-----ProSerProProAlaPro----- 102
Db 391 ACTCTCTCTCTCTGTCGCAATGATGACCGCAACAGAACCAATGGCGGAAACACAC 450
Qy 103 -----SerValProGlyProProSerAsnProSerArg-----GluGlyGly 116
Db 451 AGAGACGGCTCCACACCATCACCGCTCGTCAGGAACAGAACTTCCGGTGAAGGCGG 510
Qy 117 SerProArgProProSerSerProSerProSerSerSerSerSerSerGlySerThr 136
Db 511 TCACCTTCACCACTCGGTGCGTGAAGGCCCTCCTCAGAAATAGTGAGATTCAGACTCA 570
Qy 137 -----GlyValValValGlyIleAlaIleGlyGlyVal 147
Db 571 TCGGTAATCATCCACAAGCCAACTTGGATTGATTATGGAGTCTTGTAGGACGAGG 630
Qy 148 AlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAsp 167
Db 631 CTTTGTCTTCTACTTGCAGTGTATTGTCATCTGTTTGCACAGGAGAGAGAGAGAA 690
Qy 168 GluGluAspAla-----TyrTyrValProProProProProProGlyProLysAla 184
Db 691 TCTCTCAGGTCAACACATGCACTACTACTACAAATCAATCAATCTTATGGAGGACCCCTCA 750
Qy 185 Gly----- 185
Db 751 GGTAAATTACAGTTAGTATACTGGAATTTAATTTGTAGCCTAATGGTGTGTTGATTAGGT 810
Qy 186 -----GlyProTyrGlyGlyGlnGlnGln 194
Db 811 TTCAGAACGATCATAGTCTAATGGTTTCTGTAGCTCCATATGGCAAAAGATTAGATT- 869
Qy 195 TrpArgGlnGlnAsnAlaThr-----ProPro 203
Db 870 TATAGCTAAAGAGAGAGTTTCATAGTGTAGGTAAATGGTGTGTTATTACAAGGGAACACT 929
Qy 204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223
Db 930 CAAGATCATGTGGT-----AATATGGTGTCAAGGAGGTGGGAATGGGGTCCACAGCAA 986
Qy 224 ProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
Db 224 ProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
```

Db 987 CCTGTGTCGTCTCT-----CACAGTGATGCTTCCAACTTAACCGGT 1028  
Qy 244 ArgProValLeuProProSerProGlyLeuValLeuGlyPheSerLysThrPhe 263  
Db 1029 CGAACTGCTATACCGTCACCTCAA---GCTGCAACTCTTGCTCAACAAGCACCTTC 1085  
Qy 264 ThrTyrGluLeuLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283  
Db 1086 ACATACGATGAACCTGTCATTTGCAACAGAAAGTTTCGCTCAGTCAAAATTTGCTAGGACAA 1145  
Qy 284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303  
Db 1146 GGAGATTTGGGTATGTTTCATAGAAGGTTCTGCTAGTGCACAAAGAGTTGCGATGAG 1205  
Qy 304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluLeuLeu 323  
Db 1206 AGTCTTAACTTGAAGTGGCAAGGGGACCGAGTTTCAAGCAGAGGTTGATATCAT 1265  
Qy 324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343  
Db 1266 AGCCGTGTCATCATCGTCATCTCGTTCTCTGTTGGATATTCATCTCTGCGTGGTCAA 1325  
Qy 344 ArgLeuLeuValTyrGluPheValProAsnAsnLeuLeuGluHisLeuHis----- 361  
Db 1326 AGACTTTGGTTATGAGTTTATACCTAAACAACACTCTTGAATTTTCATCTTCATGTTACA 1385  
Qy 361 ----- 361  
Db 1386 TTCATCTAACAGATGTTTCTTGTTATTAACAAAACCTTTAAAGTATGTTTCTCTTTAAT 1445  
Qy 362 -----GlyGluGlyArgProThrMetGluTrpSerThrArgLeu 374  
Db 1446 CAGGAACATGATTGAATTTTCAGAAAGGGTTCGTCGGTTTGGATTGGCCCTACAAGAGT 1505  
Qy 374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluLeuPheCys----- 391  
Db 1506 GAAGATTCATTTGGATCAGCTAGAGGCTTGATATTTGATGAAGACTGTAGAAAAT 1565  
Qy 391 ----- 391  
Db 1566 CTTTATCTCACATATTTGTCATCAGTTTCTATCTGCTCTCTACAAATATTTGAAAGATTGT 1625  
Qy 392 -----AsnProLysIleIleHisArgAspIleLysAlaSerAs 404  
Db 1626 ATATGTTTACATCAATATAGTGCACCTTCGATTTATCCACAGAGATATCAAAAGTGCAAA 1685  
Qy 404 nIleLeuIleAspPheLysPheGluAla----- 413  
Db 1686 CATCTCTGATTTTCAGTTTGTAGAC-C-CAAGGATGATGTTGTTATATATCGACTCTGTAC 1744  
Qy 413 ----- 413  
Db 1745 TACTTTTACTTTCATGTCTCTCAATTTTGTGTTTCCATCTGTCGATGTCGTATCAGT 1804  
Qy 414 -----LysValAlaAspPheGlyLeuAlaLysIleAlaSerAspTh 427  
Db 1805 CTTATTTGTAAATATATGCAAGTGGCAGATTTTGGATTGGCTAAGCTATCTCAAGACAA 1864  
Qy 427 rAsnThrHisValSerThrArgValMetGlyThrPhe-Gly----- 440  
Db 1865 CTATACTCATGTCCTCACTCCGTCATGGGAACCTTTTGGGTAAGCAGCTTTGTAATAATGT 1924  
Qy 440 ----- 440  
Db 1925 CTCAACTCATCCACATTTATTTAGTTTCTTTCACCTGTTTGTAAATTTTCTTGATCA 1984  
Qy 441 --TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheS 460  
Db 1985 GATACTTAGCTCCAGAGTATGCATCAAGCGGAAAGTTATCCGACAAATCTCATGTTTCT 2044  
Qy 460 erPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnV 480  
Db 2045 CATTTGGAGTAAATGCTTCTTGAGCTCAATAACCGGAAGACCTCTCTTGATTAACCTGGA- 2103

Qy 480 alTyrValAspAspSerLeuValAspTrp----- 489  
Db 2104 --GAAATGGAAGATAGCTTGTTAGATTGAGTTCGGTCCCGCTCTTCGGTTTACTT 2161  
Qy 489 ----- 489  
Db 2162 GTTTAATCCCAAAACACTTTTCCAAAGCAAAACAGAAACAAATCTTACTATTGTTGTTC 2221  
Qy 490 --AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspA 509  
Db 2222 AGCAAGCCCTTTGTTGTTGAAAGCAGCTCAAGATGAGATTACACCAATTTGCTGATC 2281  
Qy 509 laLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaA 529  
Db 2282 CAGCTCTAGAGCTAAACTACAGTCATCAAGAGATGTTTCAATGGCTTCTTGTGAGCTG 2341  
Qy 529 laCysValArgHisSerAlaArgArgProArgMetSerGlnIle----- 544  
Db 2342 CAGCATCAGACATTCAGCAAGAGACGGCTTAGATGAGCCAGGT-TCAAAAAACTCATA 2400  
Qy 544 ----- 544  
Db 2401 CCACCTTGTGTTCTATTGTTATATTTTACTCACAAATTAATCTTGATGATAAATGTGAC 2460  
Qy 545 -----ValArgAlaLeuGluG 550  
Db 2461 ATACTAATGAATCTTGAACCATGTGTATGTTAAATGAAAAAGATTGTACGAGCCTAGAA 2520  
Qy 550 lYAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrS 570  
Db 2521 GAGATGTCAATGATGATCTTAAGTGAGGGAACAAGACCGGACAAAGCAGTACTTGA 2580  
Qy 570 erSerTyrGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysP 590  
Db 2581 GCCCGGGAGGTGAGTCTAGAGTATGACGCAAGCTCGTACACGGCAGACATGAAAAAGT 2640  
Qy 590 heArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGlyTyrSerAsnProT 610  
Db 2641 TCAAGAACTGGCGTTAGAGAAATAAAGATATCAAGCAGT--GAATATGCTGGA---A 2694  
Qy 610 hrSerAspTyrGlyLeuTyrProSerGlySerSerGluGlyGlnThrThrArgGluM 630  
Db 2695 CAAGTAGATGCTTAAACCCCTCTGCTTCAAGTAGTGAA-----GAAA 2739  
Qy 630 etGluMetGlyLysIleLysArgThrGlyGln 640  
Db 2740 TGAATAGAGCTCAATGAAACGCAATCCTCAG 2771  
RESULT 12  
ID ACF36552  
ACF36552 standard; DNA; 2820 BP.  
AC ACF36552;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Arabidopsis PERK1 receptor related protein encoding DNA.  
XX  
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
XX wound; pathogen resistance; plant growth; seed production; gene; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W02003072763-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-FEB-2003; 2003WO-CA000274.  
XX  
PR 28-FEB-2002; 2002CA-02373903.  
XX  
PR 28-FEB-2002; 2002US-00086464.

PA (GORI/) GORING D.  
PA (SILV/) SILVA N.  
PA (HAFF/) HAFFANI Y Z.  
XX  
PI Goring D, Silva N, Haffani YZ;  
XX  
DR WPI; 2003-712727/67.  
DR P-PSDB; ABR82941.  
XX  
PT Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase  
PT activity.  
XX  
PS Disclosure; Fig 13; 123pp; English.  
XX  
CC The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents a PERK1 polypeptide related protein encoding genomic  
CC DNA from A. thaliana (Accession NO. CNA18823)  
XX  
SQ Sequence 2820 BP; 819 A; 630 C; 576 G; 795 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3,42e-35 Length: 2820  
Score: 1471.50 Matches: 366  
Percent Similarity: 49.89% Conservative: 99  
Best Local Similarity: 39.27% Mismatches: 152  
Query Match: 42.62% Indels: 318  
DB: 9 Gaps: 28

US-10-086-464-2 (1-647) x ACF36552 (1-2820)

QY 1 MetSerAlaProSerProGlyThrGlySerProProSerProSerProSerThr 20  
DB 52 GTGGATTTCATCTCTCCCTGAAACC---TCAAAATGGGACACCCGCTCAACGGAACA 108  
QY 21 ThrThrProProProAlaSerAlaProProProThrThrProSerSerProPro 40  
DB 109 TCG-----CCGTCTAATGAGTCATCGCGCGCAACACACCTTCTTCACCACCA 159  
QY 41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaPro 60  
DB 160 TCATCA-----ATATCTGCTCTCGCCGAGATATCTCGCTTCTTTTCACCGCG 210  
QY 61 ProSerProProThr-----ProSerThrProGlySerProProProLeu 75  
DB 211 CTGCACCAACCAACGGAACAGTCACCTCTCTACATCTCCGCTCATCGCGCGCTGT 270  
QY 76 -----ProGln-----ProSerProProAlaPro-----Thr 84  
DB 271 GTAGCTAATCCGTCACCGCAGACTCCAGAGATCTCTTCTCCACCTGCACCTGAAGGCTCA 330  
QY 85 ThrProGlySerProProAla---ProValThrPro-----ProThrArgAsn 99  
DB 331 ACTCTGTAAACGCCACTGCACCAACCAACACCGTCGAACCAATCACCAGAAAGCA 390  
QY 100 ProProPro-----ProGln-----ProSerProProAlaPro----- 102  
DB 391 ACTCTCTCTCTCTCTGTCCTCAATGATGACCGAAGCAACCAATGCGGGAACCAAC 450  
QY 103 -----SerValProGlyProProProSerAnProSerArg-----GluGly 116  
DB 451 AGAGACGGCTCCACACCATCACACCGCTCGTCAGGGAACAGAACTTCCGGTGCGTGC 510

QY 117 SerProArgProProSerProSerProProSerProSerSerAspGlyLeuSerThr 136  
DB 511 TCACCTTCACCACTCGGTGCGTAAGCCCTCTCAGAAATAGTGAGATTTCAGACTCATCA 570  
QY 137 -----GlyValValValGlyIleAlaIleGlyGlyVal 147  
DB 571 TCGGTAATCATCCACCAAGCAATTTGAGATTGATTTAGGATCTCTTGGAGCAGCG 630  
QY 148 AlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgAsp 167  
DB 631 CTTTGTCTTCTTACTTGCAGTGTGATTTGCATCTGTTCGAAACAGGAAGAAAGAA 690  
QY 168 GluGluAspAla-----TyrTyrValProProProProProGlyProLysAla 184  
DB 691 TCTCTCAGGTCAACCATGCACTACTACATAACAATCTTATGGAGGACCCCTCA 750  
QY 185 Gly----- 185  
DB 751 GGTAAATTACAGTTTAGTATACTGGAATTTAATTTGTAGCCTAATGTTGATTAGGT 810  
QY 186 -----GlyProTyrGlyGlyGlnGlnGln 194  
DB 811 TTCAGAACGATCATAGTCTAATGTTTCTGTAGCTCCATATGGCAAAAGATTAGATT- 869  
QY 195 TrpArgGlnGlnAsnAlaThr-----ProPro 203  
DB 870 TATAAGCTAAAGGAGATGTTGCATAGTGTAGTAAATGTTGTTTATACAGGAACACCT 929  
QY 204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223  
DB 930 CAAGATCATGTGTG----AATATGGTGGTCAAGAGGTGGGAATTTGGGGTCCACAGCA 986  
QY 224 ProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243  
DB 987 CTTGTGCTGTGCTCT-----CACAGTGTGTTTCCACTTACCTTACCGGT 1028  
QY 244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263  
DB 1029 CGAACTGCTATACCTGTCACCTCAA---GCTCAACTCTTGTGTCAACCAAGCACTTTC 1085  
QY 264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283  
DB 1086 ACATACGATGAAGTCTCCATTCGCAACAGAGAGTTTCGCTCAGTCAAAATTTCTAGGACA 1145  
QY 284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303  
DB 1146 GGAGATTGGGTATGTTTCATAAAGGAGTCTGCTAGTGCAAGAAAGTTGCGATGAAG 1205  
QY 304 GlnLeuLysValGlySerGlyGlnGlyArgGluPheGlnAlaGluValGluIle 323  
DB 1206 AGTCTTAACTTGGAAAGTGGACAGGGAACGCGAGTTTCAAGCAGAGGTTGATATCAT 1265  
QY 324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343  
DB 1266 AGCGGTGTCATCATCGTCATCTCGTTTCTCTGTGATATTCATCTCTCGTGGTCAA 1325  
QY 344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis 361  
DB 1326 AGACTTTGGTTATGAGTTTATACCTAACCAACTCTTGAATTTTCATCTTCATGGTACA 1385  
QY 361 ----- 361  
DB 1386 TTCATCTAACAGATGTTTCTTGTATTAAACAAACCTTTAAGTATGTTTCTCTTTAAT 1445  
QY 362 -----GlyGluGlyArgProThrMetGluTrpSerThrArgLeu 374  
DB 1446 CAGGAACATGATTGAAATTTTCAGGAAGGTCGTCGGTTTGGATTTCGCTACAAGAGT 1505  
QY 374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys----- 391  
DB 1506 GAAGATTGCATTGGATCAGCTAGAGGCTTGATATTTGATATTTGATGAAAGACTGTGAAGAAAT 1565



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Db 158 ACACGCGCGTGTGACAGACCATCCACTCTCTCTCCAGATTTCACAGCTTCCTCTTACCT 217
Qy 29 -----AlaProProProThrThrProSerSerProProPro 40
Db 218 TCGATTCTTCTCCGCTAACAGATTCTCCACCTCCACCTTCGGATTCTTCTCCACCCGTT 277
Qy 41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaPro--- 59
Db 278 GATTCAAC---CCATTCCGCGCGCACCGAGCTCAACAGCAATCTCTCTCTCTCCAGAA 334
Qy 60 -----ProProSerProProProProProSerProProGlySerProProPro--- 74
Db 335 GATTCCGAAACACACCTCTCTCCCAATGAATCAATGACAAACACCTCTCTCCGCT 394
Qy 75 -----LeuProGlnProSerProProAla-----ProThrThrPro 86
Db 395 CAAGATCTTCAATCGCTCTCTCATCGTCGCGCGTCCGCAATGTAGGACCCACAAACCCG 454
Qy 87 GlySerProPro-----AlaProValThrProProThrArgAsnPro-----Pro 101
Db 455 GAATCACCACCGTTTACATCTCTCCAGCTCCACCAGCATCAGATCTTACAAATTCACCG 514
Qy 102 ProSerValProGlyProProSerAsnPro-----SerArgGluGlyGlySerPro 118
Db 515 CCAGCTTCACCATTAGACCTTACCAATCTCTCCCAATACCAATACCATCAGGACCGACCT 574
Qy 119 ArgProProSerSerPro-----SerProProSerPro-----SerArgGluGlyGlySerPro 129
Db 575 TCTCTCCGCGTAATCTCCAAACGCTCCGCGAGCCCAATTCCTCCACAGTACCAACCCAAAAC 634
Qy 129 -----TyrValPro 175
Db 635 CCTTCTAGTGGACCTGGTGTCTCCATCTCTCACATCCCCTAGTAAAGAACTCCTACT 694
Qy 130 -----SerSerAspGlyLeuSerThrGly-----ValVal 139
Db 695 CCAAAACCAAGCAATGAGATGGCGTGGCGGTGGTGGCGGTATCAAGGGAAGACTATG 754
Qy 140 ValGlyIleAlaIleGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeu 159
Db 755 GTTGTATGGCTGTAGCGGTTTCGAATCTGCGCGCTTATAGCGCTTATAGCGCTGTGTCTTAGTG 814
Qy 160 CysLysLysLysArgArgArgAspGluGluAspAlaTyr-----TyrValPro 175
Db 815 AGAAGAAAGAAAGAGA-----AACATTGATAGCTATATCATCTCAGTACTTGCCA 868
Qy 176 ProPro-----TyrValPro 175
Db 869 CATCCCAATTTCTGTGTTAAATCAGGTTTAAATAATCTCACCTTTATCTCTCTCTGATCAT 928
Qy 177 -----TyrValPro 175
Db 929 CTTCTATGCTGTTGAATCATCTCTCTGACTATCTTTGCTTTGATGTAGATGATTCCTTA 988
Qy 178 -----ProProProGlyProLysAlaGlyGlyProTyrGlyGlnGlnGln 194
Db 989 TAGCGTCAAGATCCAGGTAAAGGATCTCTCTGCTCTTAATGGTTCAATGATATAACAAT 1048
Qy 195 TrpArgGlnAlaAlaThrProProSerAspHisValValThrSerLeuProProPro 214
Db 1049 TCACAGCAACAACAATCTCTTATGGGAAACAGTATATGGTACAGCTGGT----- 1096
Qy 215 ProLysAlaProSerProProGlnProProProProProProProPheMetSer 234
Db 1097 -----GGTGGTTATCTCATCATCA-----ATGCAA 1123
Qy 235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProProProGlyLeu 254
Db 1124 TCAATGGGCACACCTGAC-----TCTGCT 1147
Qy 255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274
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Qy 489 ----- 489
Db 2286 AACTTTCAACATCTTCAATAATAGTAGAATGGCCCTAGTACTATATATAGTACTTA 2345
Qy 490 -----AlaAtpProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGlu 504
Db 2346 TAAATGAACCTCACAGCGCGCCCTCTTCTCAAGCCATTGAGACCGGAGATTTAAGC 2405
Qy 505 GlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVal 524
Db 2406 GAACTGATTATACACGGCTTGAAGCGTTATGTGGAGCATGAAGTCTTCAGATATGATC 2465
Qy 525 AlaCysAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln--- 543
Db 2466 GAGACAGCGCGTGCATGTGTAGACATCTCTGTCCTCAAAACGCCACGCATGGTTCAAGTA 2525
Qy 543 ----- 543
Db 2526 ATTCTGACTAACCAAAAGTCCAAAGCTCCCATATATATAGTAACAAGTATTTCTCACATCT 2585
Qy 544 -----IleValArgAlaLeuGluGlyAsnValSerLeu 554
Db 2586 GAAAACTTATCTACTCTTCGAAATAAGTTGTGAGACATTGGACTCGCGAGACTCG 2645
Qy 555 SerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGly 574
Db 2646 GGAGATATTAGCAACGGAATCAAAATTGGGCAA----- 2678
Qy 575 SerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysPheArgLysMetAla 594
Db 2679 AGCAACAATTATGACTCAGGGCAATACAATGAAGACATTATGAATAATCAGGAAATGGCG 2738
Qy 595 LeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
Db 2739 TTTGGTGTGTATACAGGTAGACTCAGGATTGTACAGT-----GGA 2780
Qy 615 LeuTyrProSerGlySerSerGlu 623
Db 2781 AACTACTCTGCCAAAGCTCTTCAGAT 2807

RESULT 14
ACF36550
ID ACF36550 standard; DNA; 2880 BP.
AC ACF36550;
XX
XX 18-DEC-2003 (first entry)
XX
XX Arabidopsis PERK1 receptor related protein encoding DNA.
XX
XX PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
XX wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
XX Arabidopsis thaliana.
XX
XX W02003072763-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-CA000274.
XX
XX 28-FEB-2002; 2002CA-02373903.
XX 28-FEB-2002; 2002US-00086464.
XX
XX (GORI/) GORING D.
XX (SILV/) SILVA N.
XX (HAPP/) HAPFANI Y Z.
XX
XX Goring D, Silva N, Haffani YZ;
XX
XX WPI; 2003-712727/67.
XX P-PSDB; ABR82939.
```

XX Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase  
PT activity.

XX Disclosure; Fig 11; 123pp; English.

XX The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a Proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents a PERK1 polypeptide related protein encoding genomic  
CC DNA from A. thaliana (Accession NO. AAC98010)

XX SQ Sequence 2880 BP; 814 A; 693 C; 569 G; 804 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.5e-27 Length: 2880  
Score: 1209.50 Matches: 325  
Percent Similarity: 43.85% Conservative: 92  
Best Local Similarity: 34.17% Mismatches: 160  
Query Match: 35.03% Indels: 376  
DB: 9 Gaps: 26

US-10-086-464-2 (1-647) x ACF36550 (1-2880)

Qy 2 SerSerAlaProSerProGlyThrGlySerProProSerProSerProSerProThr 21  
Db 98 AACTCAGCTTCTCCACCTGTGTGATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 157  
Qy 22 Thr-----ThrProProAlaSer----- 28  
Db 158 ACACCGCGCTGTGAGAACCATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 217  
Qy 29 -----AlaProProProThrProSerProProSerProProPro 40  
Db 218 TCGATTCTCTCCGCTAACAGATTCTCCACCTCCACCTCTCCGATCTCTCTCCACCG 277  
Qy 41 ProSerThrIleProThrSerProProSerProSerSerArgSerThrProSerAlaPro 59  
Db 278 GATTCAACC---CCTTCTCGCGCGCCACCGACGTCAAACGAATCTCTTCTCTCCAGAA 334  
Qy 60 -----ProProSerProProThrProSerThrProGlySerProProPro 74  
Db 335 GATTCCGAACACACCTCTCTCCACCAATGAATCCAATGACACACACCTCTCTCTCTCT 394  
Qy 75 -----LeuProGlnProSerProProAla-----ProThrProPro 86  
Db 395 CAAGATCTTCAATCGCT 454  
Qy 87 GlySerProPro-----AlaProValThrProThrArgAsnPro-----Pro 101  
Db 455 GAATCACACCGTTACAACT 514  
Qy 102 ProSerValProGlyProProSerAsnPro-----SerArgGluGlyGlySerPro 118  
Db 515 CCAGCTTCACCATTAGACCTTACCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 574  
Qy 119 ArgProProSerSerPro-----SerProProSerPro----- 129  
Db 575 TCTCTCTCGGTAATCCCAACGCTCCGCCGAGCCCATTCCTCCACAGTACCAACCAAACT 634  
Qy 129 ----- 129  
Db 635 CTTTCTAGTGGACCTGTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTACT 694

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QY 130 -----SerSerAspGlyLeuSerThrGly-----ValVal 139
D 695 CCAACCAAGCAATGGAGATGGCGGTGGCGGTATCAAGGGNAGACTATG 754
QY 140 ValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeu 159
D 755 GTTGTATGGCTGTAGCGGTTTCGAATCATGGCGCTTATAGGGGTTGTCTTAGTG 814
QY 160 CysLysLysLysArgArgAspGluGluAspAlaTyr-----TyrValPro 175
D 815 AGAAGAAAGAAAGAGA-----AACATTGATAGCTATAATCACTCAGTACTTGCCA 868
QY 176 ProPro----- 177
D 869 CATCCCAATTTCTCTGTTAAATCAGGTTTAAAAATCTCACCTTTATCTCTCTCATCAT 928
QY 177 ----- 177
D 929 CTTCTATGTGCTTGAATCATCTCTGACTATCTTTGCTTTTGATGTAGATGGATTTCTTA 988
QY 178 -----ProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGln 194
D 989 TACGCTCAAGATCCAGGTAAAGGATCTCTCTGCTCTTAATGGTTCAATGTATTAACAAT 1048
QY 195 TrpArgGlnGlnAsnAlaThrProSerProSerAspHisValValThrSerLeuProPro 214
D 1049 TCACAGCAACAACATCTCTATGGGAACAGATTATGGTACAGCTGGT----- 1096
QY 215 ProLysAlaProSerProProArgGlnProProProProProProProPheMetSer 234
D 1097 -----GGTGGTTATCTCTCATCATCAA-----ATGCAA 1123
QY 235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProSerProGlyLeu 254
D 1124 TCAAGTGGCACACCTGC-----TCTGCT 1147
QY 255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274
D 1148 ATACTCGGAAGTGGCCAGACTCATTTAGTTACGAAGAGCTTGCTGAGATAACACAGGC 1207
QY 275 PheSerGluAlaAsnLeuLeuGlyGlnGlyPheGlyTyrValHisLysGlyValLeu 294
D 1208 TTTGTCTCGCAAAACATTTCTCGAAGAGCGGATTTGGATGTGCTATAAAGGTACATTG 1267
QY 295 ProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArg 314
D 1268 CAGGATGGTAAAGTTGTTGCGGTTAAGCAGCTTAAAGCTGGAAGTGGACAGGTGACCGT 1327
QY 315 GluPheGlnAlaGluValGluIleIleSerArgValHisArgHisLeuValSerLeu 334
D 1328 GAATTCAAAGCAGAGGTTGAGATCATCAGCCGGTTTCATCATCGCAATTTGCTCTCTG 1387
QY 335 ValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 354
D 1388 GTTGGTTACTGCATTTCAAGCACCAGCATAGATTGCTTATCTATGATGATGTTTCTTAATCAA 1447
QY 355 AsnLeuGluLeuHisLeuHisGlyGlu----- 363
D 1448 ACCTTGGAGCATCATTTGTCATGGTGAGTGACTTTGTACCATTTCGTTATAGATAAGACT 1507
QY 364 -----GlyArgProThr 367
D 1508 TTTTITTTAGCTTACGTGTTAGACTGACTCGCTTTACGCTTTTAGGNAAGGTTTGCCAGT 1567
QY 367 rMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrIle 387
D 1568 TTTTAGAGTGGTCTAAGAGAGTCCGGATCGCTATAGGATCAGGCAAGGGTTGGCATATCT 1627
QY 387 uHisGluAspCysAsn----- 392
D 1628 TCACGAAGACTGTAA--GTAAATGCCTTCACATTTTCTTAGTTGTGCTTTGTTATGCAAC 1686
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QY 393 -----Proly 394
D 1687 TTCATAGTTTAAACAGAAAGCCAAAATCATATCTCTTGTGTTTATTATTACAGGTCATCCGAA 1746
QY 394 sIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLys 414
D 1747 AATCATTCACAGAGATATAAAGTCAGCAATATTCTTCTAGATGATGAATTAAGAGCTCA 1806
QY 414 8----- 414
D 1807 -GGCAATTAATGAATCTCTCTTTCGTTAAATCTATCTTATGACTGTAAAGTTTTAGTTA 1865
QY 415 -----ValalaAspPheGlyLeuAlaLysIleAl 424
D 1866 ATGAGACTGTGTTCTGTTTTTTTGGATGTTTAGTGTGCTGATTTTGGACTTGTCTAGACTCAA 1925
QY 424 aSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe-Gly----- 440
D 1926 TGATACAAACACAAACTCATGTTTCAACTCGGGTTATGGGAACCTTCGGGTAAAGCAACAT 1985
QY 440 ----- 440
D 1986 TCATCACAAACTCTACTCCAAAACCTGGACCTTATTGTATCCAAATGCTGATGAAAGTTTG 2045
QY 440 ----- 440
D 2046 TTATATATGGCTTGAGGCAACAAATTTGGATCAAACTCGAATCTTTTATTGATCGTATGGCT 2105
QY 441 -----TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuT 453
D 2106 GCATGACATGTTTTGTGTTAAGTACCTAGCGCGGAATATGCATCAAGTGAAATAATGA 2165
QY 453 hrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgA 473
D 2166 CTGATAGATCCGANGATTTCTCATTCGSGGTGTTCTCTTAGAGCTTGTAACTGACGGA 2225
QY 473 rGProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp----- 489
D 2226 AACCAAGTTGACACAGACTCAGGCTCTAGGAGAAGAGAGTTTGGTTGAATCGGTGAAGATCC 2285
QY 489 ----- 489
D 2286 AACTTTCAACATCTTCAATAATAGTAGAAGATTGGCCCTAGTATATCTATATAGTACTTA 2345
QY 490 -----AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGlu 504
D 2346 TAAATGAAGTACACAGCGCGCGCTGCTTCTCAAGACCATTTGAGACCGGAGATTTAAGC 2405
QY 505 GlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVal 524
D 2406 GAACTGATTGATACACGGCTTGAAAAGGCTTATGTGGAGCATGAAGTCTTCAGAATGATC 2465
QY 525 AlaCysAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln--- 543
D 2466 GAGACAGCGCTGTCATGTTAGACATTTCTGTGTCAAAACGCCACCGCATGTTTCAAGGTA 2525
QY 543 ----- 543
D 2526 ATTCTGACTAACCAAAAGTCCAAAGCTCCCATATATAGTAAAGTGATTTCTCACATCT 2585
QY 544 -----IleValArgAlaLeuGluGlyAsnValSerLeu 554
D 2586 GAAAACTTATCTACTCTTCGAAATAAGGTTGTGAGAGCATTTGAGCTGCGACGAGACTCG 2645
QY 555 SerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGly 574
D 2646 GGAGATATTAGCAACGGAATCAAAATTGGCAA----- 2678
QY 575 SerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysPheArgLysMetAla 594
D 2679 AGCACAACTTATGACTCAGGGCAATACAATGAAGACATTATGAATTCAGGAAATGGCG 2738
QY 595 LeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
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Db 2739 TTTCGGTGGTATACACGGTAGACTCAGGATTGTACAGT-----GGA 2780  
Qy 615 LeuTyrProSerGlySerSerGlu 623  
Db 2781 AACTACTCTGCCAAAGCTCTTCAGAT 2807  
RESULT 15  
ACF36553  
ID ACF36553 standard; DNA; 3060 BP.  
XX ACF36553;  
AC ACF36553;  
XX 18-DEC-2003 (first entry)  
DT Arabidopsis PERK1 receptor related protein encoding DNA.  
DE PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
KW wound; pathogen resistance; plant growth; seed production; gene; ds.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX WO2003072763-A1.  
PN 04-SEP-2003.  
PD 28-FEB-2003; 2003WO-CA000274.  
XX 28-FEB-2002; 2002CA-02373903.  
PR 28-FEB-2002; 2002US-00086464.  
XX (GORI/) GORING D.  
PA (SILV/) SILVA N.  
PA (HAFF/) HAFFANI Y Z.  
XX Goring D, Silva N, Haffani YZ;  
PI WPI, 2003-712727/67.  
XX P-PSDB; ABR82942.  
PT Producing a transgenic plant having an increased plant resistance, plant  
PT growth or seed production comprises transforming a plant with a nucleic  
PT acid molecule having a proline-rich Extensin-like Receptor Kinase  
PT activity.  
XX Disclosure; Fig 14; 123pp; English.  
XX The invention relates to producing a transgenic plant having increased  
CC plant height, number of branches, number of seed pods and/or seed  
CC production compared to a non-transgenic plant, and/or quicker flowering  
CC or later senescence compared to a non-transgenic plant. The method  
CC involves transforming a plant with a vector including a proline-rich  
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
CC acid molecule having PERK activity. The method, as well as the PERK  
CC nucleic acid molecule and polypeptide, are useful in increasing plant  
CC resistance to wounding and pathogens and in increasing plant growth and  
CC seed production. The nucleic acid molecule and polypeptide may also be  
CC used in producing transgenic plants or transgenic host cells. The present  
CC sequence represents a PERK1 polypeptide related protein encoding genomic  
CC DNA from A. thaliana (Accession NO. CAA18550)  
XX  
SQ Sequence 3060 BP; 797 A; 766 C; 592 G; 905 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 8.1e-27 Length: 3060  
Score: 1185.00 Matches: 342  
Percent Similarity: 39.28% Conservative: 72  
Best Local Similarity: 32.45% Mismatches: 185  
Query Match: 34.32% Indels: 456  
DB: 9 Gaps: 31  
US-10-086-464-2 (1-647) x ACF36553 (1-3060)

Qy 2 SerSerAlaProSerProGlyThrGlySerProPro----- 13  
Db 43 TCTTCTCGCGCTCGGCACT---TCCCGCGTGCATGTACCTCGGCAGAT 99  
Qy 14 -----SerProSerAsnSerThrThrThrThrThrProProAla. 27  
Db 100 TCGGTACCTGACAGTCATCACCTCCAGCTCCTCTTGTCTCTCTTCCCTCCCACTTG 159  
Qy 28 SerAlaProProThrThrProSerSerPro----- 39  
Db 160 AGCTCTCTCGCG---TTGCGCTTACCACCGCTCTCTCCGCTCCACCGCTTCCCA 216  
Qy 40 -----ProProSerThrIleProThrSerProProProSerSer 52  
Db 217 CCGCTCTTCCGGTTGAATCCCGCGCTCTCTCTATAGAAATCACCGCTCTCTCTA 276  
Qy 53 ArgSerThrProSerAlaProPro-----ProSerProThrPro-----Ser 67  
Db 277 CTGGAATCAGCT 336  
Qy 68 ThrProGlySerProProLeuPro-----GlnProSerProProAlaPro 83  
Db 337 GCTCTCTCGGTTTCCCGCTTACCTTCTTCCCGCAACCTCTCTCTCTCTCTCT 390  
Qy 84 ThrThrProGlySerProProAlaProValThrProPro-----ThrArgAsnProPro 101  
Db 391 -----CCTTCTTCCAGCTCTCGAGACAGTTTCCCGCGGAAATACGATTTCTCCACCA 444  
Qy 102 Pro-----SerValProGlyProPro 108  
Db 445 CCTCGTTACTTCTCTCGGAATCAACCCCGCGGTGAACACAGCTTCTCTCTCCACCGCA 504  
Qy 109 SerAsnProSerArgGluGlyGlySerProArgPro----- 120  
Db 505 TCTCTCTCTCGCGCGGTAGTGGC---CCTAAGCCTTCGTTCTCTCTCTCTCTCTCT 561  
Qy 121 ---ProSerSerProPro----- 126  
Db 562 TCTCCACCAATCTTCTCTCGAATCACTCCGTAACCTTCTCTCTCTCTCTCTCTCT 621  
Qy 127 ---ProSerProSer----- 131  
Db 622 CCACCGCTCTAAGACGCAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 681  
Qy 132 -----AspGlyLeu----- 134  
Db 682 GCAGCAGTAACTCTCTCTTCTTGGCGCAGCGGCAATTTACCGATGGACCGTAGCA 741  
Qy 134 ----- 134  
Db 742 CCTCTATTGGCGCTGTTATAGAGCCAGACGAGTCCAGCGCAATCAATATCTCTCGGGA 801  
Qy 135 -----Ser 135  
Db 802 ACCGCACAGCACTGGTTCCGAAGTCTACCTGTACGAGCTGTATACCGATCATATCC 861  
Qy 136 ThrGlyValValValGlyIleAlaIleGlyValAlaLeuLeuValIleValThrLeu 155  
Db 862 GCGGATTTCTTATTGGCGGTGAATCGTTGGAGCTCTTCTACTAATTTCTGTAGGCTT 921  
Qy 156 IleCysLeuLeuCysIleLysLysArgArgAspGluGluAsp-AlaTyrTyrValPr 175  
Db 922 CTCTTTGTCTTCTACAGAGCTACCAAGAAATAGAAATTAACAACAGAGCTCTGCTCATCAT 981  
Qy 175 oProProProPro----- 180  
Db 982 CAATCCAAACTCCCTCAAAAGTATAAACTTTGAGATCAATTTGTTTACAGCTGCTCACT 1041  
Qy 181 -----GlyProLysAlaGlyGlyProTyrGlyGlnGlnGlnGlnTpar 196  
Db 1042 TAAATGTATGTAAATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 1101  
Qy 196 GlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuProProProPro 216

Db	1102	GGCGGTAATGCTGGTACGAACACGACATGTTATCACA---ATGCCACCAACAATCCA	1158
Qy	216	sAlaProSerProProArgGlnProProProProProPheMetSerSerSe	236
Db	1159	TGCTAAA-----TATATATCTAG	1176
Qy	236	rGlyGlySerAspTyrSerAspArgProValLeuProProProSerProGlyLeuValle	256
Db	1177	TGGAGGTGTGATACGAAGGAGAAC-----AATTCGTTCGCAAAAACAT	1221
Qy	256	uGlyPheSerLysSerThrPheThrTyrGluLeuAlaArgAlaThrAsnGlyPheSe	276
Db	1222	TTCAATGCCATCTGGAATGTTCTCCTACGAAGAACTTTCAAAAGCAACTCGTGGATTTTC	1281
Qy	276	rGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSe	296
Db	1282	AGAGGAGAACCTTTTGGAGAGAGCGGTTCCGGATATGTTACAAAGGAGCTGTTGAAAA	1341
Qy	296	rGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPh	316
Db	1342	CGGACACAGAAGTTGCGGTGAAGCAGCTGGAAGATTGGGAGCTATCAAGGGGAAAGAGAAT	1401
Qy	316	eGlnAlaGluValGluLeuIleSerArgValHisHisArgHisIeuValSerLeuValGl	336
Db	1402	CCAAGCTGAGGTGGACAACTCAGTAGGGTTCATCAAGCAGCTCGTTTCATTTGGTTGG	1461
Qy	336	YTyrcyIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLe	356
Db	1462	TTATTGGCTTAATGGAGATAAAGACTCTGGTTTACGAGTTGGTTCCTAAAGATACCTT	1521
Qy	356	uGluLeuHisLeuHisGly-----	362
Db	1522	GGAGTTCCACTTGCATGGTAAATAGATATATGATTTTCATCTCTTTTGTGTTCTTTA	1581
Qy	362	-----GluGlyArg--ProThrMetGl	369
Db	1582	GTTCAATTATGTTGAGTATTGTGAGATATATGTTGTAGAGAACAGAGGAAGCGTGTGGA	1641
Qy	369	uTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGl	389
Db	1642	ATGGAAATGAGGCTCAGGATTGCTGTAGGAGCAGCAAAAGGATTAGCTTATCTTCATGA	1701
Qy	389	uAspCys-----	391
Db	1702	GGATTGTGAGTGTCTCTTCATAATGGGAATGGAACAAATGCCTTTTTCGGGTTTTCGAC	1761
Qy	392	-----AsnProLysIleIleHisArgAspIl	400
Db	1762	ACTGATATTGATTTCTGGTGCTTGATATGAGGAGCTCCAACATAATTCACCGTGNAT	1821
Qy	400	eLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLys-----	414
Db	1822	CAAAAGCAGCTAATATCTCTCTAGATTCCAAATTTGAGGCCAAAGGTGATCTGCTTTTAAT	1881
Qy	414	-----	414
Db	1882	CTTATCAAAAGTTGGTTTTTAGAACAAGAGTTTGCCCAATTTTCGGTTTATAGTCACACCAT	1941
Qy	415	-----ValAlaAs	417
Db	1942	TTTGTTCTATTAAACAAGATTACATGTAGCTTAGAGTTCTTGTTCTCTTCAGGTCTCTGA	2001
Qy	417	pPheGlyLeuAlaLysIleAlaSerAspThrAsn-----ThrHisValSerThrAr	434
Db	2002	CTTTGGACTAGCCAAAGTTTTTCTCTAGATCCAAATTCATCATTCATCATATCTCTACTCG	2061
Qy	434	gValMetGlyThrPheGly-----	440
Db	2062	AGTGSTAGGAACCTTCGGGTAAACAACCATCCATCCATGCTTTATATGTTGTGTGTCATTGT	2121
Qy	440	-----	440

Db	2122	GTTTAAAAATATTAATTTACGGTTTTCAAGTTTTCAAGTTTTCAAGTTTTCAAGTTTTCTTCCTT	2181
Qy	440	-----	440
Db	2182	GTTGTATCGTAATCCAGATCAAAAGATTTATTGATTACTAAATGCCTTTGTGCACCGTCT	2241
Qy	441	-----TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuTh	453
Db	2242	ATTTGGTATGCATTTAAACAGATACATGGCTCCAGAAATACGCGTCCAGTGGTAAAGTAAC	2301
Qy	453	rGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgAr	473
Db	2302	TGATAAATCAGATGATATTCCTTTGGGGTGGCTTCTAGAACTCATCACTGGACGCTCC	2361
Qy	473	gProValaspAlaAsnAsnValTyrValaspSerSerLeuValaspTrp	489
Db	2362	ATCAATTTTCGCCAAAGATTCTTCCACAAACCAGAGTTTAGTAGACTGGGTAAAGTCAAAG	2421
Qy	489	-----	489
Db	2422	TACATGATGATGATGATACCATTAGGTTTTCTTTTCCCCTAGTTATTAGATGAAA	2481
Qy	489	-----	489
Db	2482	ATGAAACTCCAGTATAACTCGAAGCTTGAACCTCATTAGACTGTAAATTTTGATTATTC	2541
Qy	490	-----AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla	508
Db	2542	CTCAGGCGAGGCCATTGCTTACGAAAGCAATCTCTGAAAGAAAGTTTGTGACTTCTTCGTAG	2601
Qy	508	spAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla	528
Db	2602	ACTCAAGGTTGGAGAAGAAATTACGATACAACTCAGATGGCAACAATGGCTGCTTGTCGTG	2661
Qy	528	laAlaCysValArgHisSerAlaArgArgProArgMetSerGlnIle	544
Db	2662	CTGCTTGATACGCCAATCAGCTGGCTTCGGCTCTAGAAAGAGCCAGGT-CTGAGATTAA	2720
Qy	544	-----	544
Db	2721	GTTTAAATACATGTATTTCGTCCATATATCGAAGAGGAAACGCTAATCCATCAATACAT	2780
Qy	545	-----ValArgAlaLeuGluGlyAsnValSerLeuS	555
Db	2781	TTATATCTTGAAAAAACTTGAATAGGTAGTACGTCTCTTGAAGGCGAGGTGGCCCTGA	2840
Qy	555	erAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlyS	575
Db	2841	GAAAGGTCGAAG------ACTGGAAATAGCGTACCTAGTCTCTCTGAAAACC	2891
Qy	575	erThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaL	595
Db	2892	CGAATGCATC--ACACCACGGTATGGAACAATAAGAGGAGATTCTC-----	2935
Qy	595	eUGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyL	615
Db	2936	-----GACACAGGTTCAACCGATGGTTACACTTCAAGATTATCGAG	2975
Qy	615	eutyProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysI	635
Db	2976	TTAACCTTCTCAGTCGAGCAGTGAACATCAACAGGTGAATACTTAGTTCCACAGGTTCAA	3035
Qy	635	leLysArgThrGlyGlnGlyTyrSerGlyProSerLeu	647
Db	3036	TA-----GGGCAAGTTTCACCCACAATTAA	3058

Search completed: April 24, 2004, 22:22:00  
Job time : 666 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2004, 20:30:41 ; Search time 133 Seconds  
(without alignments)  
2699.648 Million cell updates/sec

Title: US-10-086-464-2  
Perfect score: 3453  
Sequence: 1 MSAPSPTGSPSPSPNST.....REMEMGKIKTGQYSGPSL 647

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Deiop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued\_Patents\_NA -QPMT=fastap -SUFFIX=X-rni -MINWATCH=0.1 -LOOPCL=0  
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- 2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PTCUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	756	21.9	3239	4	US-09-228-986-9
2	744.5	21.6	1593	4	Sequence 9, Appli
3	740	21.4	2868	4	Sequence 1, Appli
4	712	20.6	1488	4	Sequence 4, Appli
5	703.5	20.4	2513	4	Sequence 13, Appli
6	678	19.6	2432	4	Sequence 7, Appli
7	667.5	19.3	1559	4	Sequence 3, Appli
8	604.5	17.5	4104	3	Sequence 1, Appli
9	602	17.4	1224	4	Sequence 3, Appli
10	600.5	17.4	3097	4	Sequence 11, Appli
11	581.5	16.8	3590	1	Sequence 1, Appli
12	581.5	16.8	3590	4	Sequence 1093, Ap

13	581.5	16.8	3590	5	PCT-US96-09193-1	Sequence 1, Appli
14	578	16.7	2114	4	US-09-602-472A-5	Sequence 5, Appli
15	575	16.7	2749	1	US-08-265-628-1	Sequence 1, Appli
16	572	16.6	2571	1	US-07-717-331F-9	Sequence 9, Appli
17	572	16.6	2833	1	US-07-717-331F-1	Sequence 1, Appli
18	567	16.4	1554	2	US-08-587-680A-24	Sequence 24, Appli
19	566.5	16.4	2389	4	US-09-228-986-1	Sequence 1, Appli
20	562	16.3	2336	4	US-09-228-986-10	Sequence 10, Appli
21	559.5	16.2	2638	4	US-09-228-986-8	Sequence 8, Appli
22	546	15.8	2749	1	US-07-717-331F-4	Sequence 4, Appli
23	545	15.8	966	1	US-08-447-185-2	Sequence 2, Appli
24	545	15.8	2443	1	US-08-447-185-3	Sequence 3, Appli
25	543	15.7	2686	4	US-09-228-986-3	Sequence 3, Appli
26	531.5	15.4	5733	2	US-08-473-553A-1	Sequence 1, Appli
27	486	14.1	2943	4	US-09-503-922-2	Sequence 2, Appli
28	460.5	13.3	2649	4	US-09-228-986-12	Sequence 12, Appli
29	430	12.5	2568	4	US-09-228-986-2	Sequence 2, Appli
30	401	11.6	1926	4	US-09-249-585A-2	Sequence 2, Appli
31	401	11.6	1926	4	US-09-410-399-3	Sequence 3, Appli
32	401	11.6	2580	3	US-09-050-863-2	Sequence 2, Appli
33	401	11.6	2580	4	US-09-359-081-2	Sequence 1, Appli
34	401	11.6	5452	2	US-09-130-114-1	Sequence 1, Appli
35	401	11.6	8705	4	US-09-647-344A-14	Sequence 14, Appli
36	401	11.6	9600	3	US-08-910-647-1	Sequence 1, Appli
37	401	11.6	9600	4	US-09-620-925-1	Sequence 1, Appli
38	401	11.6	10596	1	US-07-884-811-15	Sequence 15, Appli
39	401	11.6	10596	1	US-07-885-971-15	Sequence 15, Appli
40	401	11.6	10596	1	US-08-087-783A-15	Sequence 15, Appli
41	401	11.6	10596	1	US-08-194-088B-15	Sequence 15, Appli
42	401	11.6	10596	2	US-08-194-087-15	Sequence 15, Appli
43	401	11.6	10596	5	PCT-US93-04648-15	Sequence 15, Appli
44	401	11.6	16080	4	US-09-724-566A-48	Sequence 48, Appli
45	395.5	11.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-228-986-9  
; Sequence 9, Application US/09228986  
; Patent No. 6359198  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling  
; FILE REFERENCE: 11000/1020  
; CURRENT APPLICATION NUMBER: US/09/228,986  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 3239  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-228-986-9

Alignment Scores:  
Pred. No.: 1.88e-23  
Score: 756.00  
Percent Similarity: 51.93%  
Best Local Similarity: 34.99%  
Query Match: 21.89%  
DB: 4  
Length: 3239  
Matches: 190  
Conservative: 92  
Mismatches: 132  
Indels: 130  
Gaps: 17

US-10-086-464-2 (1-647) x US-09-228-986-9 (1-3239)

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Qy 108 oSerAsnProSerArgGluGlySerProArgProProSerSerProProSe 128

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Db 1828 -----GCCATAGCAAAAGGTGTATGATGTGGATCGCTATTGGCGGCACCGT 1874
Qy 148 aleuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysLysArgArgAspG 168
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Db 2026 -----TTCTC 2030
Qy 264 rTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAenLeuLeuGlyGlnG 284
Db 2031 CTATGATGAATTAAGAGGTGCACCAATAATTCTCCGATACCAATGAATTAGGCTTCG 2090
Qy 284 yGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysG 304
Db 2091 AGGATACGGAAAGGTGTACAGGGAGGATCTTCTCGATGCTCATATATAGCAATCAAAAG 2150
Qy 304 nLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleLeSe 324
Db 2151 AGCTCAGCAGGGGTCTATCGAGGGTGCAACCGAGTTCAGACAGAAATCGAGCTCTTC 2210
Qy 324 rArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysAr 344
Db 2211 GCGGGTTCATCAACAAGATCTTGTTGGCCTCATAGGATTCGTTTCGAGCAGGAGACGA 2270
Qy 344 gLeuLeuValTyrGluPheValProAsnAsnLeuLeuGluLeuHisLeuHisGlyGluG 364
Db 2271 GATGTGGTCTATGAATATATATCCTAACCGGACGCTCAGGGATAGCTTGACAGGAAATC 2330
Qy 364 yArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLe 384
Db 2331 AGGCATTTATCTTGATTTGAAGAGAGGCTTGATAGCTCTAGGTTTCGCTAGAGACT 2390
Qy 384 uSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAs 404
Db 2391 AGCTTATCTGCAGCAACTCGCAATCTCCCAATTATCCACAGAGATGTCAAGTCCACCAA 2450
Qy 404 nIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAl 424
Db 2451 TATCTTGTGGACGAACATCTGACGCGCCAAAGTCGCGGATTTTCGGTTTTCGCAAACTGT 2510
Qy 424 aSerAspThrAenThr---HisValSerThrArgValMetGlyThrPheGlyTyrLeuAl 443
Db 2511 ATCGACACCGGGAAGGGGACGTTTCGACGCAAGTGAAAGGACGCTGGGCTATTGGA 2570
Qy 443 aProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVa 463
Db 2571 TCCCGAATACTACATGAGTCAACAGCTGACAGAAAGAGCGATGTGTACAGCTTCGGGT 2630
Qy 463 lValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAenAsnValTyrValAs 483
Db 2631 GGTCTAGCTTGAGCTCATCTGCAAGCAACCGATTTGAGAGAGGGGCAAGTATGTCTGTCG 2690
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Qy 483 pAspSerLeuValAspTTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPh 503
Db 2691 CGAG-----ATTCGACCCCATCGACAGAACGACAG-----GACTA 2729
Qy 503 eGlyGly-----LeuAlaAspAlaLysMetAsnAsn---GlyTyrAspArgGluG 519
Db 2730 CTACGGCGTGAAGGAATATGATGGACCCGCTCCATGAGGAGCATGGCTAC---CTCGTCGG 2786
Qy 519 uMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPr 539
Db 2787 GTTCAGCAGGTTCTTGGATTTCGGCATGCGATGTGTCAGGAGTCGGCTCGCGACCCGCC 2846
Qy 539 oArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnG 559
Db 2847 CACATGAGCGAGGTGTGAAGCGATCGACCATGTTGCAG-----AACGA 2894
Qy 559 uGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAs 579
Db 2895 TGGGATACACACCAACTCGAGTCGGCATCGCTCGTCG-----GCGACGGACTTTGG 2945
Qy 579 pSerSerGln-----TyrAsnGluAspMetLysLysPheArgLysMe 593
Db 2946 GTCGACGAAGGCGCTCCTCGCATCCGTACACGATCGCTTACCCAAG----- 2994
Qy 593 tAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTy 613
Db 2995 -----NAGGAAGTTAGCTATAGGATTCCTTTGATTATAGT-----GGTGGATA 3038

RESULT 2
US-09-602-472A-1
; Sequence 1, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guohua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
;
US-09-602-472A-1

Alignment Scores:
Pred. No.: 2,9e-23 Length: 1593
Score: 744.50 Matches: 172
Percent Similarity: 57.07% Conservative: 66
Best Local Similarity: 41.25% Mismatches: 116
Query Match: 21.56% Indels: 63
DB: 4 Gaps: 9

US-10-086-464-2 (1-647) x US-09-602-472A-1 (1-1593)
Qy 235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProSerProGlyLeu 254
Db 181 TCGTCGGGTTCGAAAGACGGGTTCGACGGGTTCAGATT----- 216
Qy 255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274
Db 217 -----GCTGCTCATACATTCTTTCGGGAGCTTGACGCTGCAACAAACAAT 264
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**Qy**    588 LysLysPheArgGlySerMetAlaLeuGlyThrClnCluTyrHenAlaThrGly    604  
Db      1333 GAAAAAAGACGACAAGAATGCACAGGCCGTTTTGATGGGAATGCTAACCGT    1383

**RESULT 3**

US-09-228-986-4 .  
; Sequence 4, Application US/09228986  
; Patent No. 6359198  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Niels  
; TITLE OF INVENTION: Compositions isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling  
; FILE REFERENCE: 11000/1020  
; CURRENT APPLICATION NUMBER: US/09/228,986  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 2868  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
**US-09-228-986-4**

Alignment Scores:

Pred. Score.:                 7,71e-23                 Length:                 2868  
Score:                  740.00                 Matches:                 182  
Percent Similarity:        50.91%                 Conservative:            69  
Best Local Similarity:     36.92%                 Mismatches:             133  
Query Match:                21.43%                 Indels:                  109  
DB:                                  4                 Gaps:                    13

**US-10-086-464-2 (1-647) x US-09-228-986-4 (1-2868)**

**Qy**    90 ProAlaProValThrProProThrArgAsnProProSerValProGlyProPro--- 108  
Db      858 CCATGTCGGGATCTCTCCCTTTTCCTCCTCTCCCTCTCATCACCCCCGCCAGTA 917

**Qy**    109 -----SerAsnProSerArgGlucgLyserProArgProProSerSerProSerPro 126  
Db      918 GCTGGAGCAATGGAGCAGGGTCGAGACTCTCCC----- 953

**Qy**    127 ProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaileGlyGly 146  
Db      954 -----AGCACAGGACCATTGCTGGGGAGTAGTGCAGGT 989

**Qy**    147 ValAlaLeuLeuValIllevalThrLeulleCysteuleuCySlysLysLysArgargarg 166  
Db      990 GCTGCCCTCTATT----- 1004

**Qy**    167 AspGluGluAspAlaTyrtYrvlProProProProProGlyProLysAlaGlyGly 186  
Db      1005 -----GCAGTCTCTGCAATTGGGTTCT 1025

**Qy**    187 ProTYrGlyGInGInGInTrpArgGlnGlnAsnAlaThrProProSerAsphis 206  
Db      1026 GCCTGG-----TSGCGTCGCAGAAAG-----CCACAGAGCAC 1058

**Qy**    207 ValValThrSerLeuProProProPolysAlaProSerProProArgGlnProProPro 226  
Db      1058 ----- 1058

**Qy**    227 ProProProProPhoMeMetSerSerSerGlyGlySerAspTYrSerAspArgProVal 246  
Db      1059 -----TICTTTGATGACTCTGCT 1076

**Qy**    247 LeuProProProSerProGlyLeuValLeuglyPheSerLYSSerThrPheThrGlu 266  
Db      1077 -----GAGGAGGATCCAGAAGTTCATTAGCCCACTTAG--AGGTTCTCATTCAGG 1127

**Qy**    267 GluLeualaArgAlaThrAnsnGlyPheSerGluaLaAsnLeuLeuGlycndGlyPhe 286  
Db      1128 GAATTCAGGTTTGCACCTGATGGTTTTTAGCAATAAGAAAACATCTTGGCAGAGGTGGTTTT 1187

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QY 207 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
DB 1188 GGAAGGGTGAACAAGGCGCTTCAGATGTTCTTGGTGGCTGTAAACGTCGAG 1247
QY 307 ---ValGlySerGlyGlnGlyLysGluPheGlnAlaGluValGluLeuIleSerArg 325
DB 1248 GAAGAGCGTACACCGGGTGGAGAGTTCAGTTTCAACAGAGTGGAGATGATGAAGCATG 1307
QY 326 ValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeu 345
DB 1308 GCAGTACATAGAACCTCTTCGATCTAGTGTGATTTCTGCATGACACCCCACTGAACGGCTG 1367
QY 346 LeuValTyrGluPheValProAsnAsnLeuGlu-----LeuHisLeuHisGlyGlu 363
DB 1368 CTGTGTTATCCCTACATGCCCAATGGAAGTGTGCTTCATGCTACGAGAGGGCCACA 1427
QY 364 GlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
DB 1428 AATGACCCACCTTAGATTGGCCAACTCGCAAGCGCATAGCATTTGGTTCGCAAGAGGT 1487
QY 384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
DB 1488 CTCCTCTACTGATGATCATTTGTCATCTAGATTTATTCACCGGATGTCGAAGCTGCT 1547
QY 404 AsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423
DB 1548 AACATCTTACTGGATGAAGAATATGAGGAGTGTGGGGGATTTTGGCTTGGCAAACTT 1607
QY 424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443
DB 1608 ATGGATTATAAGACACACATGTTACGACGGCTGTTCTGGTGAACCATTTGGCCACATAGCA 1667
QY 444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463
DB 1668 COTGAGTACCTTCTACTGGAAGTCTTCGGAAGAGACAGACGATTTTGGATATGGAATC 1727
QY 464 ValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnValTyrValAsp 483
DB 1728 ATGTTGCTGGAACTATTATACGGGACACAGGGCATTTGACCTTGACCGTTAGCAAAATGAT 1787
QY 484 AspSer-----LeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGly 501
DB 1788 GATGATGTCATGTTGCTTACTGCTGCTTAAAGGCTACTA-----AAAGAGAGA 1835
QY 502 AspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAla 521
DB 1836 AGGCTTGATATGCTAGTTGATCCTGATCTTAAGAACAAATTATGTTGAACGACAGAGTGGA 1895
QY 522 ArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgProArgMet 541
DB 1896 CAACCTATTCAAGTTGCATTACTTTGTACACAGGGTCAACCAATGGATAGACCAAGATG 1955
QY 542 SerGlnIleValArgAlaLeuGluGlyAsn-ValSerLeuSerAspLeuAsnGluGlyMet 561
DB 1956 TCTGAAGTGGTAAGGATGTTGGAAGGGATGCTTAGCTGAGAGATGGGAGGAATGGCAA 2015
QY 561 tArgProGlyGlnSerAsnValTyrSerSerTyrGly 573
DB 2016 AAGG-----TGAAGTCTGACGGA 2034

RESULT 4
US-09-579-182-4
; Sequence 4, Application US/09579182
; Patent No. 6500628
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-161
; CURRENT APPLICATION NUMBER: US/09/579,182
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 7
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/ SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-182-4

Alignment Scores:
Pred. No.: 6,04e-22 Length: 1488
Score: 712.00 Matches: 178
Percent Similarity: 53.07% Conservative: 73
Best Local Similarity: 37.63% Mismatches: 160
Query Match: 20.62% Indels: 62
DB: 4 Gaps: 14

US-10-086-464-2 (1-647) x US-09-579-182-4 (1-1488)

QY 205 AspHisValValThrSerLeuProPro-----ProProLysAlaProSer 219
DB 22 GAACACACGATAAATCCCTTCGCTCCGCTATATTTCTTAAATCCGATAAATCAAGTCT 81
QY 220 ProProArgGlnProProProProProProProPheMetSerSerSerGlyGlySer 239
DB 82 -----CGACAGGTCCT----- 93
QY 240 AspTyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSer 259
DB 94 -----GNAACAGAGAGGAGCTAAGTCTCCAAAGAGAGGCGCTACTGCGCATATTGCT 147
QY 260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279
DB 148 GCACAAACCTTTACTTTCCGAGAGTGTAGTCCGCCACTAAAAACTTTTCGACCGGAATGT 207
QY 280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu---ProSerGlyLys 298
DB 208 CTTCTTGAGAGAGGAGGTTTCGGACGTTTACAAAGGTCGTCTAGAGACCACAGGACAG 267
QY 299 GluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAla 318
DB 268 ATAGTAGCTGTAAACAGCTTGTATCGAAACGCTCTACAAGGAAACACAGAGAGTTTCTGTA 327
QY 319 GluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCys 338
DB 328 GAGGTTCTTATGCTGAGCCTTCTGCATCATCCCACTTTGTAATTTGATTTGTTATTGT 387
QY 339 IleAlaGlyAlaLysArgLeuValTyrGluPheValProAsnAsnLeuGluLeu 358
DB 388 GCTGATGGGACCGCGTCTTCTTGTGATGAGTATATGCCACTAGGATCATTTGGAGGAT 447
QY 359 HisLeuHisGly-----GluGlyArgProThrMetGluTrpSerThrArgLeuLysIle 376
DB 448 CATCTACACGATCTTCCACCTGATAAAGAGGCTCTAGACTGGAGTACTAGAAATGACAATA 507
QY 377 AlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIle 396
DB 508 CGCGCAGGAGCAGCAGAAAGGAGCTGGAGTATCTGCATGATAAAAGCGAATCCGCTGTGATC 567
QY 397 HisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAla 416
DB 568 TACAGAGACCTGAAATCATCCAAACATTTCTTCGGTGATGGCTATCACCCAAAGTTATCT 627
QY 417 AspPheGlyLeuAlaLysIleAlaSer---AspThrAsnThrHisValSerThrArgVal 435
DB 628 GATTTTGGTTAGCTAAGTTAGTCCCGTGGCGCATATAAACACATGTGTCAACTCGTGTG 687
QY 436 MetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLys 455
DB 688 ATGGGCACATATGGTTATTGTGCACCGGAATATGCCATGACAGGGCAACTCATCATGAA 747
QY 456 SerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVal 475
DB 748 TCCGATGTTTATAGCTTTTGGGGTGTGTCTTCGAGCTCATCACGGGTTCGAAAGCTATT 807
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Qy 476 AspaalaenValTyrValAspSerLeuValAspTTPAlaAargProLeuLeuAsn 495
Db 808 GATAATGCTCGAGCACC CGGAGACCAACCTTTCGCATGGCTAGCGCGTTTC--- 864
Qy 496 ArgAlaserGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyr 515
Db 865 -----AAAGATCGTAGNAAGTTCCGNAGATGGCGGATCCATCGTGCAGGGCGGTAT 918
Qy 516 AspArgGluGluMetAlaAargMetValAlaCysAlaAlaCysValAargHisSerAla 535
Db 919 CCAATGCGTGTCTATATCAAGCACTTCGAGTTCGAGCAATGTCTTTACAGGAACAAGCA 978
Qy 536 ArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSer 555
Db 979 GCGACAAGACCACTGATTTGGCGAGTGGTGACGCTCTAAACATACTTAGCTTCGCAAAAG 1038
Qy 556 ---AspLeuAsn-----GluGlyMetArgProGlyGlnSerAsnValTyr--- 569
Db 1039 TTTGACCCNAACGCCACCNAAGCGGTCAAAACAGTAGAAGTGGGAGTGGGCCACCATTTATC 1098
Qy 570 -----SerSerTyrGlyGlySerThrAspTyrAsp----- 579
Db 1099 AGAACAGGGATGATCGGAGGAGCTTGGGAGATGGGAGTAGCTTGGATAGTCTCGCAGAG 1158
Qy 580 -----SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMet 593
Db 1159 ACTCGGAGTCGTTAGGTACCAAGCCACTCACAGAACTCTCTGATTACAGGAAGG 1218
Qy 594 AlaLeuGlyThrGlnGluTyrAsnAlaThrGlnGlyGluTyrSerAsnProThrSer- 611
Db 1219 GATATG---GTGAGGAAGTCAATGCAGGATCAGAGTGGGAGCGGAGACAGGAGCGGG 1275
Qy 612 -----AspTyrGlyLeuTyrProSerGlySerSerSerGlyGlnThrThrArg 628
Db 1276 TCAGTAGAAAAATGGGATTA-----AGCGATTGGGAAGGCGCAAGATCAACAG 1323
Qy 629 GluMetGluMetGlyLysIleLysArgThrGlyGlnGly 641
Db 1324 AGAGGAGCGCGCGAGTGTGGGAGATCATCGAGAGC 1362
RESULT 5
US-09-228-986-13
; Sequence 13, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-13
Alignment Scores:
Pred. No.: 2,21e-21 Length: 2513
Score: 703.50 Matches: 178
Percent Similarity: 49.52% Conservative: 81
Best Local Similarity: 34.03% Mismatches: 179
Query Match: 20.37% Indels: 85
Db: 4 Gaps: 14
US-10-086-464-2 (1-647) x US-09-228-986-13 (1-2513)
Qy 84 ThrThrProGlySerProProAlaProValThrProThrArgAsnProProSer 103
Db 795 ACTGTCCTGCTCTCTCTCCCGCCACCATATATCAACCT----- 833
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Qy 104 ValProGlyProProSerAsnProSerArgGluGlyGlySerProArgProProSerSer 123
Db 834 -----CCACCTTCTAAC-----AATCGGCCACCAAGTCC 863
Qy 124 ProSer-----ProProSerProSerSerAspGly-----Leu 134
Db 864 TCAATATGCTGCTCCCTTCATCAGGTGGCTCAAGGGTGGGAACACCAATAGAAATCTCTG 923
Qy 135 SerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThr 154
Db 924 AGTGGTGGTCCCATAGTGGGTATAATATTTCAGCTTATTTGAGCTGTTGCTGCTATA 983
Qy 155 LeuIleCysLeuLeuCysLysLysArgArgArgAspGluGluAspAlaTyrTyrVal 174
Db 984 TTAGGAGTTATTTATATGACGTAAGTCTCTAGAAAGAGAGCAGGAT----- 1031
Qy 175 ProProProProProGlyProLysAlaGlyGlyProTyrGlyGlnGlnGlnGln 194
Db 1032 -----GAAGAAAAAACA 1043
Qy 195 TrpArgGlnGlnAsnAlaThrPro-----ProSerAspHisValValThrSerLeuPro 212
Db 1044 AGCAATCGTGTGCTTTTCCACCCCTATCTCCCTCGATGCTGAATATTGGAAGAGAGT 1103
Qy 213 ProProProLysAlaProProProProArgGlnProProProProProProPhe 232
Db 1104 CCAGAGCAAAAGTCAGCTCATCACCTCTTGAATCGCTCTTAAGCCCTCCCTCTTCTGAA 1163
Qy 233 MetSerSerSerGly-----GlySerAspTyrSerAspArgProValLeu 247
Db 1164 CGCAACAGGTCTACAGGGGACAAAGCTTCGGAAGTATTTTTTCAAGTAGAGGACTAAA 1223
Qy 248 ProProProProProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
Db 1224 AACCCA-----ATATCAGCAACTGAATATTCTTATTGCGAGAC 1259
Qy 268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuGlyGlnGlyGlyPheGly 287
Db 1260 CTGCAAAATGGCAACAAATAGTTTGTAGTCAAGATAATCTTATTGCGAGGGTCTCTTGG 1319
Qy 288 TyrValHisLysGlyValLeuProSerGlyGluValAlaValLysGlnLeuLysVal 307
Db 1320 CGAATCTACCGAGCAGAGTTCACAAAGGCTTGGCAGTGAAGATTTTGGCAGTGAAGAA 1379
Qy 308 Gly-----SerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleSerArg 325
Db 1380 TCTACGCTGCTCCCTACAAAGGCTGAGAGCTTCTCGACGCGAGTATCTAATATATCGGC 1439
Qy 326 ValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeu 345
Db 1440 CTACATCATCTTAACATTACAGAACTAGTGGGTATTGTCACAGAACATGAGCAATACCTT 1499
Qy 346 LeuValTyrGluPheValProAsnAsnAsnLeu-----GluLeuHisLeuHisGlyGlu 363
Db 1500 CTGTGTATGAATATTTTCGACAAATGGATCTCTATGACGTATTGACATGCGAGATGAG 1559
Qy 364 GlyArgProThrMetGluTyrSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
Db 1560 ACTACTAGAAATTTGCTTGGACATTCGTGTAAGATTCGCTGGGTGGTTCAGCTCGAGTT 1619
Qy 384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
Db 1620 TTAGAGTATTTCATGAAGTTGCTCTCCATCTTATGTCATATAAAAAAATTCAGTCGCT 1679
Qy 404 AsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423
Db 1680 AATATTTTGTGTATGATGATTTCAACCTCGTCTGTCGAGCTGTGAATTCGCG- 1733
Qy 424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443
Db 1734 GCCCTCAATCCAAATTCGACCGTCAGGTCAGGTGCTGGGTTCATTTGGGTACAGTCT 1793
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; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)...(1319)
US-09-602-472A-3

Alignment Scores:
Pred. No.: 4,39e-20 Length: 1559
Score: 667.50 Matches: 165
Percent Similarity: 57.50% Conservative: 65
Best Local Similarity: 41.25% Mismatches: 117
Query Match: 19.33% Indels: 57
DB: 4 Gaps: 9

US-10-086-464-2 (1-647) x US-09-602-472A-3 (1-1559)

Qy 219 SerProArgGlnProProProProProProPheMetSerSerSerGlyGly 238
Db 131 TCACCAAAAGTCGGCCATGAAGTCCACCCAT-CCGCCCTT----- 171
Qy 239 SerAspTyrSerAspArgProValLeuProProProSerProGlyLeuVal----- 255
Db 172 -----CCAAATTTCAGATTATCTTCGGGGTGTAGATGATGAAGA 213
Qy 255 ----- 255

214 CGAAGAACAAATGTTAATAATGCTGCTAGCTTAAGAGGGAGTCATCAGGCGCGCGGATG 273
Qy 256 LeuGlyPheSerLysSerThrPheThrTyrgluLeuAlaArgAlaThrAsnGlyPhe 275
Db 274 CTCAA-ATCGCGGCACAAACCTTCACATTCGGCAGCTTGCGCGCCGCCCAATAATTTT 332
Qy 276 SerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu--- 294
Db 333 CAGCCTGATTGCTTCTTAAGGGAGGGTGTGTTGGTGTATATAGAGGACGCTTCAG 392
Qy 295 ProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArg 314
Db 393 AGTAGTGTCAAGTTGTAGCTGTTAAACAGCTGGATGAAATGCAATGCAAGGTAACCGT 452
Qy 315 GluPheGlnAlaGluValGluLeuLeuSerArgValHisArgHisLeuValSerLeu 334
Db 453 GAGTTTCTGTTGAAGTTCTTATGCTCAGCCTTTTACATCATCCAAACTTGGTCAATTG 512
Qy 335 ValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 354
Db 513 ATTGCTACTGCGTGCAGGTGACCAAGACTCTTGTCTATGAGTTTATGCGCTTGGGT 572
Qy 355 AsnLeuGluLeuHisLeuHisGly-----GluGlyArgProThrMetGluTrpSerThr 372
Db 573 TCCTTGAAGATCACCTTCATGATGTTCCGCGCTGACAGAACCAATAGATTGG-ACA 629
Qy 373 -ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAs 392
Db 630 CAGATGAAGATAGCGGCTGT-CCAGCCAGGGGTGGAGTTCTTCATGATAAAGCTAA 688
Qy 392 nProLysIleHisArgAspIleLysAlaSerAsnIleLeuLeuAspPheLysPheGly 412
Db 689 CCCACCAAGTTATTCGGGACTCAATCATCAACATTTGCTGATGAGGATTTCA 748
Qy 412 uAlaLysValAlaAspPheGlyLeuAlaLysIleAla---SerAspThrAsnThrHisVa 431
Db 749 ACCAAAGCTGTCGACCTCGGCTCGGAAACTGGGCCCACTGGAGCAAGTCTCATGT 808
Qy 431 lSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLy 451
Db ----- 451
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Db 809 TTCCACACGGGTGATGGGTACATACCGTTACTGTGCTCTCCAGTATGCCATGCTGTCA 868
Qy 451 sLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuThrGly 471
Db 869 GTTAAACGGTCAAATCCGATGTGTACAGCTTTGGTGTGCTCTTTTACAGCTTATTACCG 928
Qy 471 YArgArgProValAspAlaAsnAsnValTyrValAspSerLeuValAspTTPAlaA 491
Db 929 TAGAAAAGCCATAGATAGCACTCAACACATGGACAGACACCTGGTGACATCGGCACG 988
Qy 491 gProLeuLeuAsnArgAlaSerGluGlnGlyArgPheGluGlyLeuAlaAspAlaLysMe 511
Db 989 ACCTTTGTTCAAC-----GACAGAAGAAATTCACATCGTTGGTGACCCACCGGTT 1039
Qy 511 tAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysVa 531
Db 1040 AGAAGGTGCGGTACCAATGCGGGGCTGTACAGCGCTAGCGGTGGCATCCATGTGTAT 1099
Qy 531 lArgHisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAs 551
Db 1100 TCAAGAACAGGTTGCAGCCCGGCTTTGATTGCTGACGTGTAACTCGCTATCTTATCT 1159
Qy 551 nValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSer-----As 567
Db 1160 TGCA-----AACCGGGGTAGATCCGAC-CACAGCTCCAGCTTCATAA 1203
Qy 567 nValTyrSerSerTyrGlySerThrAspTyrAspSerSerGlnTyrAsnGluAsp 586
Db 1204 CATCATCAGCAGCGCGCGCAAGGAGAGACTTTAAACCGCAAGGTTTTCGAAAAAAC 1261

RESULT 8
US-08-881-706-1
; Sequence 1, Application US/08881706
; Patent No. 6245969
; GENERAL INFORMATION:
; APPLICANT: Chong, Joane
; TITLE OF INVENTION: Receptor Kinase BIN1
; FILE REFERENCE: 07251/022001
; CURRENT APPLICATION NUMBER: US/08/881,706
; CURRENT FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4104
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(3687)
US-08-881-706-1

Alignment Scores:
Pred. No.: 4,4e-17 Length: 4104
Score: 604.50 Matches: 161
Percent Similarity: 47.21% Conservative: 84
Best Local Similarity: 31.02% Mismatches: 148
Query Match: 17.51% Indels: 127
DB: 3 Gaps: 14

US-10-086-464-2 (1-647) x US-08-881-706-1 (1-4104)

Qy 107 ProPro-----SerAsnProSerArgGlyGlySerProArgProProSer 122
Db 2350 CCACCGGCTAAGTCTTGAACAATCTCGGCTC---TGTTGTTATCTCTTCGCGGTGT 2406
Qy 123 SerProSerProProSerProSerSerAspGlyLeu-----SerThrGly 137
Db 2407 GATCCTTCA-----AATGCAGACGGTTATGCTCATCATCAGATCTCATGGA 2454
Qy 138 ValValGlyIleAlaIleGlyGlyValAlaLeuValIleValThrLeuIleCys 157
Db 2455 AGGAGACCGGCTCCCTTGTGTTAGTGTGGCGATGGATGTGTTCTCTTTTGTGTGT 2514
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Qy 236 SerGlyGlySerAspTyrSerAspArgProValLeuProProProSerPro-----Gly 253
Db 364 AAGACGATCGAGCGTATCTTCGTAATCTTTGACAGCTCCATCTCTCTTCCTGGT 423
Qy 254 LeuVal-----LeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAla 269
Db 424 CTTCCTGAGTTTCTCACCTTGGATGGGA---CATTTGGTTCACTCTTAGAGATCTTCAG 480
Qy 270 ArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyPheGlyTyrVal 289
Db 481 ATGGCTACTAATCATGTTTCAAGGATAATATCATCGGTGATCGGTGATATGAGATTGTT 540
Qy 290 HisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer 309
Db 541 TACCGCGTAACCTTGTATAGTACTCTCTCTGTTGTAATAAGTTGCTCAACAATTTA 600
Qy 310 GlyGlnGlyGluArgGlyPheGlnAlaGluValGluLeuLeuSerArgValHisArg 329
Db 601 GGACAGCTGATAAAGACTTCAGAGTTGAAGTTGAAGCTATAGTCCAGTTCGACATATA 660
Qy 330 HisLeuValSerLeuValGlyTyrCysLeuAlaGlyAlaLysArgLeuLeuValTyrGlu 349
Db 661 AACTTGGTCCGCTTCTCGGATATTTGATGAAGAAACGACAGG-----705
Qy 350 PheValProAsnAsnLeuLeuHisLeuHisGlyGlyGluGlyArgProThrMetGlu 369
Db 705 -----705
Qy 370 TrpSerThrArgLeuLysLeuAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGlu 389
Db 706 -----CTCGGCTACCTTCAGAG 723
Qy 390 AspCysAsnProLysLeuLeuHisArgAspLeuLysAlaSerAsnLeuLeuAspPhe 409
Db 724 CGCATTCAGCCAAAGTGGTGCACAGACATTAAGTCTAGTACATCTCGATTGATGAC 783
Qy 410 LysPheGluAlaLysValAlaAspPheGlyLeuAlaLysLeuLeuAspThrAsnThr 429
Db 784 AAATTCATCTTAAATTTCTGACTTTGGACTTCTAAACTACTTGGTGTGATGAAGAT 843
Qy 430 HisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSer 449
Db 844 TTTATACTACTAGATTATGGGTACCTTCGGTTACGTAGCTCCAGAGTATGCAATTC 903
Qy 450 GlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuLe 469
Db 904 GGTCTTCTGAATGAGAAAGCGATGTCTACAGCTTCGGGGTTGACTCTTGGAGCTATA 963
Qy 470 ThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp 489
Db 964 ACTGGTAGATATCCGGTAGACTATGCTCGTCCACCACCCGAGGTACATTTGGTGGAGTGG 1023
Qy 490 AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGlyGlyLeuAlaAspAla 509
Db 1024 CTGAAGATGATGTC-----CAACAAGACGATCAGAAAGTGGTTGATCCA 1071
Qy 510 LysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAla 529
Db 1072 AACCTTGAACAAACCAACCATCTACAAGTGTCTTGAAGAAAGACACATTTGCTGCTTGA 1131
Qy 530 CysValArgHisSerAlaArgArgProArgMetSerGlnLeuValArgAlaLeuGlu 549
Db 1132 TGTGTTGATCCAAATGTCTGAGAAAGACCGAGGATGAGCCAAAGTTTCACGCTGCTTGA 1191
RESULT 10
US-09-228-986-11
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
```

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; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-11
Alignment Scores:
Pred. No.: 4,95e-17 Length: 3097
Score: 600.50 Matches: 173
Percent Similarity: 46.08% Conservative: 80
Best Local Similarity: 31.51% Mismatches: 172
Query Match: 17.39% Indels: 126
DB: 4 Gaps: 13
US-10-086-464-2 (1-647) x US-09-228-986-11 (1-3097)
Qy 66 ProSerThrProGlySerProProPro-----LeuPro 76
Db 1523 CCTGCAAGTTCTGGACGCTCCAAAACACACGCTTAGACGGAGTTGTTCCCGACGCTTGGG 1582
Qy 77 GlnProSerProAlaProThrThrProGlySerProProAlaProValThrPro--- 95
Db 1583 AGAGCTGAAAGACCTTCACCTACTGGAAGTGGAGATAAAGCTGCTACAAG-GTACCTTAC 1641
Qy 96 -----ProThrArgAsnProProProSerValProGlyProPro 108
Db 1642 CAGATTCCTTGAACACAGACAGCTTGGAGGTCCAGAACTCAGGAACTTGTGCTTTCCT 1701
Qy 109 SerAsnProSerArgGluGlyGlySerProArgProProSerProSerPro----- 126
Db 1702 TCTCCACACCGGTGC-GGTGATGCATCATCTTAGTCTTCAATTGAGGACCCCAAGTT 1760
Qy 127 -----ProSerProSerAspGlyLeuSerThrGlyValValValGlyIleAla 143
Db 1761 ACAATAGTTCCCGAGAGAAACAAAGGGGACATAATCGTTTAGCCATTATATCTCGAGCA 1820
Qy 144 IleGlyGlyValAlaLeuValIleValThrLeuIleCysLeuLeuCysLeuLysLys 163
Db 1821 GTCGGAGGATATCATCTAGTATTTTACTCATCCCGCTCTCGTATTTCATGTACAGAAAG 1880
Qy 164 ArgArgArgAspGluGluAspAlaTyrTyrValProProProProProGlyProLys 183
Db 1881 AGAGGAAGAACTGAA-----1895
Qy 184 AlaGlyGlyProTyrGlyGlyGlnGlnGlnTrpArgGlnGlnAsnAlaThrProPro 203
Db 1895 -----1895
Qy 204 SerAspHisValValThrSerLeuProProProLysAlaProSerProProArgGln 223
Db 1895 -----1895
Qy 224 ProProProProProProProPheMetSerSerGlyGlySerAspTyrSerAsp 243
Db 1896 -----ATGTCATATACGAA 1910
Qy 244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
Db 1911 AGGGCAGTCGCAGACGTCGAGAAACTGGAAT-----GCAGCTAAGATTTT 1955
Qy 264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
Db 1956 TCTACAAAGAGATCAAAACAGCTACAAACACTTTAAAGAA-----GTCATTGGTCAT 2009
Qy 284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
Db 2010 GGAAGTTTGGATCCGTTGTTACCTTCCAGTTGGGAAACCTTCCAGTTGGGAAACTAGTTGCTGTGAA 2069
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QY 304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluLeile 323
Db 2070 GTGCGGTTTGATAAAACCAACTTGGTGCGAGATTCTTTTCATAAATGAGGTTCGTCTTA 2129
QY 324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
Db 2130 TCACAAGTCGCGCATCAGAACCTTCAGTCTGGAAGGATTTTGTATGAGTCGCGAGGT 2189
QY 344 ArgLeuLeuValTyrGluPheValProAsnAsnLeuLeuGluLeuHisLeuHisGlyGlu 363
Db 2190 CAGATTTTGTCTATGAATATCTACCGGTGATCACTGGGTGATCACTAATGATGATGCA 2249
QY 364 Gly-----ArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381
Db 2250 AACAGTAGGAATCTCCTAAGCTGGGTCTGTAGACTCAAGATTGCTGTGATCTGCA 2309
QY 382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401
Db 2310 AAAGGACTGGACTATCTACATAATGGAAGCAATCTCGAATCATACACGAGACATCAAG 2369
QY 402 AlaSerAsnIleLeuLeaSpPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421
Db 2370 TGCAGTAATATACTATGACAGGAGGATGAATGCAAGACTTTGGGCTCTCT 2429
QY 422 Lys-----IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
Db 2430 AAGCAATGATCCAGCCAGACGCA---ACTCAGTGACCACTGCTGTCAGGGCACAGCT 2486
QY 440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
Db 2487 CGTTACCTCGACCTGAATATTACTCCACCACTTACAGAGAAAGCGACGCTCTAT 2546
QY 460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgProValAspAlaAsnAsn 479
Db 2547 ACCTTTGGAGTTGTCTTTTGGAGCTCATCTGTGACGAGAGCCGTAAATCATTCAGA 2606
QY 480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
Db 2607 ACTCCAGATTCCTCAATTTGGTTTATGGGCAAGCCCTACTTG-----CAG 2654
QY 500 GlnGlyAspPheGluGlyLeuAlaAlaSerAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
Db 2655 GCAGGTGCATTTTGAG---ATAGTGATGAGAGTTTGGGGGAAGTTTCGATGTGGAAGC 2711
QY 520 MetAlaArgMetValAlaCysAlaAlaCysValArgHisSerAlaArgArgArgPro 539
Db 2712 ATGAGAAAGTGGCAAAATCCCTGTGAGTCTGTAGAGGGGATGCATCACTAAGGCCA 2771
QY 540 ArgMetSerGlnIleValArgAlaLeuGluGly-----AsnValSerLeuSerAspLeu 557
Db 2772 ACCATTGCACAGATACTGTCTGTCTCAAGAGGCTTACAGCATTACAGCTCTCT----- 2825
QY 558 AsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAsp 577
Db 2826 -----TATCTTGCACCTCTGGACATGTGAAC 2852
QY 578 TyrAspSerSerGlnTyrAsnGluAsp 586
Db 2853 TGAATCTACTCTGATTATACCAACAGAC 2879

RESULT 11
US-08-587-889-1
; Sequence 1, Application US/08587889
; Patent No. 5654397
; GENERAL INFORMATION:
; APPLICANT: CAO, Zhaoan
; APPLICANT: CROSTON, Glenn E.
; APPLICANT: GOEDDEL, David V.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
; TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
```

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STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,889
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-60916
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-587-889-1

Alignment Scores:
Pred. No.: 3,48e-16 Length: 3590
Score: 581.50 Matches: 208
Percent Similarity: 38.68% Conservative: 86
Best Local Similarity: 27.37% Mismatches: 239
Query Match: 16.84% Indels: 229
DB: 1 Gaps: 28

US-10-086-464-2 (1-647) x US-08-587-889-1 (1-3590)
QY 1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
Db 80 ATGGCGGGGGCGGGCGGGCGGGGAGCCGCCAGCGCCCGCGCGCCAGCACTTCTTGTA 139
QY 20 rThrThrThrProProAlaSerAla-----ProProPr 32
Db 140 GAGGTGCGCCCTGGGTCAATGTGCGCTTCTACAAAGTGATGGAGCGCCCTGGAGCCG 199
QY 32 oThrThrProSerProPro----- 39
Db 200 GACTGGTCCGATTGCGCGCCCTGATCGTGGCGGACAGCCGAGCTGGGCTGTGCGAG 259
QY 40 ----ProProSerThrIleProThrSerProProSerSerArgSerThrProSerAl 58
Db 260 CGCTCGGGGCGCGCAGCGCGCGCGCTCTGTGGCCCTGGATCAACCCGAGCCCGGTG 319
QY 58 aProProSerProPro-----ThrProSerTh 68
Db 320 GCCGACCTGTGCACATCTCTCAGCACCTCAGCACCTGCGAGCTGCTCGGCGGGGACATCA 379
QY 68 rProGlySerProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
Db 380 GCCTGGCACCTCCCGCCCGCTTCGTCGCCAGCACCACTGCCCGCA-----GG 430
QY 88 rProProAlaProValThrProThrArgAsnProProProSerValProGlyProPr 108
Db 431 CCCAGCAGCATCCCTGCACCCGCG-----AGGCCGAGGCTGGAGCCCGCGGA----- 479
QY 108 oSerAsnProSerArgGluGlyGlySerProArgProProSerProSerProSe 128
Db 480 -----AGTTGCCATCTCTCAGCTCCACTTCTC-TCCCCAGCTTT 519
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Qy 128 rProSerSerAspGlyLeuSerThrGlyValValGlyValGlyValAla 148  
Db 520 TCCAGGCTCCAGACCCATTCA----- 541  
Qy 148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgAspGly 168  
Db 541 ----- 541  
Qy 168 uGluAspAlaTyrValProProProProProGlyProLysAlaGlyProTy 188  
Db 542 -----GGGCTGAGCTCGGC----- 556  
Qy 188 rGlyGlyGlnGlnGlnTrpArgGlnGlnAsnAlaThrProSerAspHisValva 208  
Db 556 ----- 556  
Qy 208 lThrSerLeuProProProLysAlaProSerProProArgGlnProProProPr 228  
Db 557 -----CTGGTTCCAGGCCCTGCTTCCCTGGGCTCCACCGCC 594  
Qy 228 oProProProPheMetSerSerSerGlySerAspTyrSerAspArgProValLeuPr 248  
Db 595 ATCTCCAGCCCTTCTTCTACCAAGCCAGGC-----CC 627  
Qy 248 oProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyGlu----- 266  
Db 628 AGAGAGCTAGTGTCTCTCCAGGAGGCCCGCCCTCTCCGTTTGTGCGCCCTCTG 687  
Qy 267 -GluLeuAlaArgAlaThrAnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyPh 286  
Db 688 TGAGATTTCGGGGCCACCCACAATTCTCGAGAGCTCAAGATCGGGAGGGTGGCTT 747  
Qy 286 eGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLy 306  
Db 748 TGGGTGGTGTACCGGGCGGTGATG--AGGAACACCGGTGTATGCTGTGAAGAGCTGAA 804  
Qy 306 aValGlySerGly-----GlnGlyGluArgGluPheGlnAlaGluValGluI 322  
Db 805 GGAGAACCGCTGACTGGAGTGGAGTGCAGTGAACGAGAGCTTCTGACCGAGGTGAGCA 864  
Qy 322 eIleSerArgValHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAl 342  
Db 865 GCTGTCAGGTTTCGTACCCAAACATTGGACTTGTGCTGGCTACTGTGCTCAGAACGG 924  
Qy 342 aLysArgLeuLeuValTyrGluPheValProAsnAsnLeuGlu-----LeuHisLe 360  
Db 925 CTTCTACTGCTGTGTAGGCTTCTTCTGCCCAACGGCTCCCTGAGGACCGTCTCCACTG 984  
Qy 360 uHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySe 380  
Db 985 CCAGACCCAGGCGCTGCCACCTCTCTCTGGCCCTCAGCGACTGGACATCTCTTGGGTAC 1044  
Qy 380 rAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspI 400  
Db 1045 AGCCCGGGCAATTGAGTTTCTATCTCAGGAC--AGCCCGAGCTCATCTCAGAGACAT 1101  
Qy 400 eLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLe 420  
Db 1102 CAAGAGTTCACACCTCTCTCTGGATGAGAGGCTGACACCCCAAGCTGGGAGACTTTGGCT 1161  
Qy 420 uAlaLysIle-----AlaSerAspThrAsnThrHisValSerThrArg-- 434  
Db 1162 GGCCCGGTTCAGCGCTTTTCCGGGTTCAGGCCCGCCAGCCAGCAGCATGTGGCGCGGAC 1221  
Qy 435 -----ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLe 452  
Db 1222 ACAGACAGTGGGGGACCTTGGCTTCTCTCCGAGAGGTACATCAAGACGGGAGGCT 1281  
Qy 452 uThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyAr 472  
Db 1282 GGCTGTGGACACGACACCTTTCAGCTTTGGGGTGTAGTCTAGACACCTTGGCTGGTCA 1341  
Qy 472 gArgProVal-----AspAlaAsnValTyrValAspAspSerLeuValAspTr 489

Db 1342 GAGGCTGTGAAGACGACCGTGCCAGGACCAAGTATCTGAAGAC---CTGGTGGAA-- 1396  
Qy 489 pAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAl 509  
Db 1397 -----CAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAACCCAGAG 1440  
Qy 509 aLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAla----- 525  
Db 1441 CACACTGCAAGCAGGCTGTGGCTGCAGATGCTGGGCTGCTCCCATCGCCATGAGATCTA 1500  
Qy 525 ----- 525  
Db 1501 CAAGAAGCACTGAGACCCAGGCCCGGCCCTGCCACCTGAGCTGGGCTGGGCTGGG 1560  
Qy 526 ---CysAlaAlaAlaCysValArgHisSerAlaArgArgProArgMetSerGlnI 544  
Db 1561 CCAGCTGGCTGTGCTGTGCTGCACCGCCGGCCCAAGGAGGCTCTCTATGACCCAGT 1620  
Qy 544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564  
Db 1621 GTACGAGAGGCTAGAG-----AAGCTGCAGGAGTGTGGGGGGTG---CCGG 1668  
Qy 564 Y-----GlnSerAsnValTyrSerSer-- 571  
Db 1669 GCATTTGGAGCGCGCCAGCTGCATCCCTTCCCGCAGGAGAACTCTTACGTGTCCAG 1728  
Qy 572 -----TyrGlySerThrAspTyrAsp----- 579  
Db 1729 CACTGGCAGAGCCACAGTGGGCTGTCTCATGCGAGCCCTGCGAGCGCCATCAGGAGC 1788  
Qy 580 -SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGl 599  
Db 1789 CAGTGGCCAGGACGAGCAGCAGTGTGACAGAGGCGCCCAACAGCCCGTGGAGAGTGACGA 1848  
Qy 599 uTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer-- 618  
Db 1849 G-----AGCCTAGCGCGCTCTCTGCTGCCCTCGCTCTGGCCTTGTACTTCAAGCTG 1902  
Qy 619 -----GlySerSerSerGlyGlnThrThrArgGl 629  
Db 1903 CCCTCTGAGCCAGCACCCCTCAGGAGGCGCGGTGTCTCAGGGGAGCACGCG-AGGAG 1961  
Qy 629 uMetGluMetGly-----LysIleLysArgThrGlyGlnGlyTyrSerGlyPro 645  
Db 1962 AATCAGCTGGGGAGTGGCGCCAGGATCCCGGCCACAGCCGTGGAAGGACTGGCCCT 2019

RESULT 12  
US-09-016-434-1093  
; Sequence 1093, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:





557 -----CTGTTTCCAAAGCCCTGCTTCCCTGTGTGCTCCACCGCC 594  
Qy  
228 oProProPheMetSerSerGlyGlySerAspTyrSerAspArgProValLeuPr 248  
Db  
595 ATCTCCAGCCCTTCTTACCAAGCAGGC-----CC 627  
Qy  
248 oProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu----- 266  
Db  
628 AGAGAGCTCAGTGTCCCTCTCAGGAGCCCGCCCTCTCGTWTGTGTGCCCCCTCTG 687  
Qy  
267 -GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPh 286  
Db  
688 TGAGATTTCCCGGGGCACCCACCACTTCTCGAGGAGCTCAAGATCGGGAGGGTGGCTT 747  
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286 eGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLy 306  
Db  
748 TGGGTGCGGTACCGGGCGGTATG---AGGAACACGGGTGTATGCTGTGAAGAGGCTGAA 804  
Qy  
306 sValGlySerGly-----GlnGlyGluArgGluPheGlnAlaGluValGlu1 322  
Db  
805 GGAGAACGCTGACCTGGAGTGACTGCAGTGAAGCAGAGCTTCTTGACCGAGGTGAGCA 864  
Qy  
322 eileSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAl 342  
Db  
865 GCTGTCCAGGTTTCGTACCAACCAATTTGCTGACTTTGCTGGCTACTGTGCTCAGAACGG 924  
Qy  
342 alySargLeuLeuValTyrGluPheValProAsnAsnLeuGlu-----LeuHisLe 360  
Db  
925 CTTTACTGCTGTGTGTACGGCTTCTGCCCCAACGGCTCCCTGGAGGAGCCGTCTCCACTG 984  
Qy  
360 uHisGlyGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySe 380  
Db  
985 CCAGACCCAGCGCTGCCACCTCTCTCTGGCTCAGCGACTGGACATCTTCTGGGTAC 1044  
Qy  
380 rAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp1 400  
Db  
1045 AGCCCGGGCAATTAGTTTCTACATCAGGAC---AGCCCCAGCCTCATCCATGGAGACAT 1101  
Qy  
400 eLysAlaSerAniLeuLeuAspPheLysPheGluAlaLysValAlaAspPheGlyLe 420  
Db  
1102 CAAGATTTCCAAAGTCCTTCTGTGATGAGAGGTGACACCAAGCTGGGAGACTTTGGCT 1161  
Qy  
420 uAlaLysIle-----AlaSerAspThrAsnThrHisValSerThrArg-- 434  
Db  
1162 GSCCGGTTTCAGCGCTTTGCGGGTCCAGCCAGCAGCAGCATGGTGGCCCGGAC 1221  
Qy  
435 -----ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLe 452  
Db  
1222 ACAGACAGTGGCGGCGCCCTGCTTACCTGCGCCGAGGAGTACATCAAGACGGGAAGCT 1281  
Qy  
452 uThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyAr 472  
Db  
1282 GGCTGTGGACAGGACCCCTTACGCTTTGGGTGGTGTAGTGTAGAGACCTTGGCTGGTCA 1341  
Qy  
472 GArgProVal-----AspAlaAsnAsnValTyrValAspAspSerLeuValAspTr 489  
Db  
1342 GAGGCTGTGAAGACCGCCAGCGTCCAGGACCAAGTATCTGAAAGAC---CTGTGTGAA-- 1396  
Qy  
489 pAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAl 509  
Db  
1397 -----GAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAG 1440  
Qy  
509 aLysMetAsnAsnGlyTyrAspArgGluGluMetAlaAla----- 525  
Db  
1441 CACACTGCAAGAGGCTGGCTGCAGATGCCCTGGGCTGCTCCCATCGCCATCGCATCTA 1500  
Qy  
525 ----- 525  
Db  
1501 CAAGAAGCACCTGGACCCCGGGCCCTGCCACCTGAGCTGGGCTGGGCTGGG 1560  
Qy  
526 ----CysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln1 544  
Db  
1561 CCAGCTGGGCTGTGCTGCTGCA CCGCGGGGCAAAAGAGGCGCTCTCTATGACCCAGGT 1620

544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProG1 564  
Db  
1621 GTACGAGAGGTAGAG-----AAGCTGCAGCACTGGTGGGGGGTG---CCCGG 1668  
Qy  
564 Y-----GlnSerAsnValTyrSerSer-- 571  
Db  
1669 GCATTGTGAGGCGCCAGCTGCATCCCCCTTCCCGCAGGAGAACTCCTACGTGTCCAG 1728  
Qy  
572 -----TyrGlyGlySerThrAspTyrAsp----- 579  
Db  
1729 CACTGGCAGAGCCACAGTGGGGCTGCTCCATGGCAGGCCCTTGGCAGGCCCATCAGGAGC 1788  
Qy  
580 -SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnG1 599  
Db  
1789 CAGTGGCCAGCAGCAGAGCAGCTGCAGAGAGGCCCAACAGCCCGTGGAGAGTGAAGA 1848  
Qy  
599 uTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer-- 618  
Db  
1849 G-----AGCCTAGCGGCGCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTG 1902  
Qy  
619 -----GlySerSerSerGluGlyGlnThrThrArgG1 629  
Db  
1903 CCCTCTGACCCAGCACCCCTCAGGAGCGCGCTGTCTCAGGGGGACACCGC-AGGAG 1961  
Qy  
629 uMetGluMetGly-----LysIleLysArgThrGlyGlnGlyTyrSerGlyPro 645  
Db  
1962 AATCGAGTGGGGAGTGGCCCGGATCCCGGCCACACAGCCGTGGAAGGACTGGCCCT 2019

RESULT 14  
US-09-602-472A-5  
; Sequence 5, Application US/09602472A  
; Patent No. 6608240  
; GENERAL INFORMATION:  
; APPLICANT: Bidney, Dennis L.  
; APPLICANT: Hu, Xu  
; APPLICANT: Li, Guihua  
; TITLE OF INVENTION: Sunflower Disease Resistance Genes  
; FILE REFERENCE: 35718/200630  
; CURRENT APPLICATION NUMBER: US/09/602,472A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/140,876  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2114  
; TYPE: DNA  
; ORGANISM: Helianthus annuus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(2114)  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1475  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1475  
; OTHER INFORMATION: n = A,T,C or G  
US-09-602-472A-5

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Score: 578.00 Matches: 143  
Percent Similarity: 55.07% Conservative: 85  
Best Local Similarity: 34.54% Mismatches: 136  
Query Match: 16.74% Indels: 51  
DB: 4 Gaps: 15

US-10-086-464-2 (1-647) x US-09-602-472A-5 (1-2114)



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Db 52 GCTGAATCTCTCTCATATTCACCAACCGTGC----- 87  
Qy 255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274  
Db 88 -----CGTCAATTTACCTTTTCGGAGATTCAACTTGCACACCCAAAC 129  
Qy 275 PheSerGluAlaAenLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu 294  
Db 130 TTTGATGAGTGGTGGTATAGGACGTTGGGGGTTTGGCAAGGTTTACAGAGGAACCTTC 189  
Qy 295 ProSerGlyLys-----GluValAlaValLysGlnLeuLysValGlySerGlyGln 311  
Db 190 ACTTATGGGGAACCATCTGTCGCAATTAAGCGCATGGAATCAGGTTCTAGTCAA 249  
Qy 312 GlyGluArgGluPheGlnAlaGluValGluLeuLeuSerArgValHisHisArgHisLeu 331  
Db 250 GGACGGTAGAGTTTAGGCTGAATTTAGATGCTCTCAATCTAAGGCACGTGTCATTG 309  
Qy 332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351  
Db 310 GTGCTTTAATTTGTTACTGCTAGTATGATGGGCAAGAGATGTTCTGTATATGAACATATG 369  
Qy 352 ProHsnAenLeuGluLeuHisLeuHisGlyGlyGluArgProThrMetGluTyrSer 371  
Db 370 CCCAATGGAACCTTTCAGATGCTCTCCAC---AAGCGTCGAGCTCTCTTAACCTTGGGTA 426  
Qy 372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHis-----Glu 389  
Db 427 AGAAGACTCAAAATATGATAGGCGCGCTCGTGGTTAGTACTTGCACACTGGTACG 486  
Qy 390 AspCysAenProLysIleIleHisArgAspLysAlaSerAenIleLeuIleAspPhe 409  
Db 487 GGTATTAACCATGAGTTATACATCGGAGTGTAAAGACACAAATATATTGTTAGATGAC 546  
Qy 410 LysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle-----AlaSerAspThr 427  
Db 547 AATTGGCGCAGCTAAGGTTTCTGACTTTGGTTTGTCCAAATTTGTCCAAACAAATCAGCCT 606  
Qy 428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447  
Db 607 TCACTTATGTTAATACCTTTGTCAGAGGACCTTTGGATATATGATCGCATTTCTT 666  
Qy 448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuGlu 467  
Db 667 CAACAGGTAGGCTGACTCGAAAGTCTGACGTGTATGCTTTGGGTTGGTCTGCTTTGAA 726  
Qy 468 LeuIleThrGlyArgArgProValAlaAsnAenValTyrValAspAspSerLeuVal 487  
Db 727 GTCCATATGTTGGAAACAAAGTAGTACTGATGAGGAGCAC-TGG-----GGTTTGGCA 776  
Qy 488 AspTyrAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507  
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Qy 508 AspAlaLysMetAenAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527  
Db 825 GATTCTAATTTAAGGGGAGAAATATCCCAAAATGTTTGAAGGAGTTTGCACACTACTAGCT 884  
Qy 528 AlaAlaCysValArgHisSerAlaArgArgProArgMetSerGlnIleValArgAla 547  
Db 885 GACCGGTGTTTGGCATAGCCGTCACCAAGCACCTCTGCAATGGCGGAGGTTGTGATTGGT 944  
Qy 548 LeuGluGlyAenValSerLeuSerAspLeuAenGluGly-----Met 561  
Db 945 CTTGAGTCAATCTTAGCTTACAGAGAAACCGAGAGTACATGGGTACCAACATTTCTC 1004  
Qy 562 ArgProGlyGlnSerAenValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 581  
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Qy 582 Gln-----TyrAsn-----GluAsp-----MetLysLysPheArgLysMet 593

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Qy 594 AlaLeu-----GlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAenProThrSer 611  
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Qy 612 AspTyrGlyLeuTyrProSerGlySerSerSerSerGlyGln 625  
Db 1176 GAT---TCCGTGTAC---AAGGGACGGCTACAAAATGGACAA 1211  
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; Sequence 1, Application US/08265628  
; Patent No. 5821094  
; GENERAL INFORMATION:  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Goring, Daphne  
; TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A  
; TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 W. Madison St. Suite 3400  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/265,628  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/959,945  
; FILING DATE:  
; APPLICATION NUMBER: US 07/847,564  
; FILING DATE: 03-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochopien Ph.D., Donald J.  
; REGISTRATION NUMBER: 32,167  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-707-8889  
; TELEFAX: 312-707-9155  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2749 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Brassica napus  
; STRAIN: oleifera  
; INDIVIDUAL ISOLATE: W1  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: S-locus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2574  
; PUBLICATION INFORMATION:  
; AUTHORS: GORING, DAPHNE  
; ROTHSTEIN, STEVEN J.  
; TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A  
; TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A  
; TITLE: FUNCTIONAL SERINE/THREONINE KINASE  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749

US-08-265-628-1

**Alignment Scores:**

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Percent Similarity:	49.80%	Conservative:	94
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Query Match:	16.65%	Indels:	91
DB:	1	Gaps:	14

US-10-086-464-2 (1-647) x US-08-265-628-1 (1-2749)

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Qy	150	LeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgAspGluGlu	169
Db	1372	CTGCTCTTATGATCATGTTCTGC---CTCTGGAAAGGAACAAAGCGAGCAAAACA	1428
Qy	170	AspAlaTyrTyrValProProProProGlyProLysAlaGlyGlyProTyrGly	189
Db	1429	ACTGCAACATCTATTGTAAT	1449
Qy	190	GlyGlnGlnGlnThrArgGlnGlnAsnAlaThrProSerAspHisValThr	209
Db	1450	-----CGACAGAGAAAC-----CAAGATTTTGGTAAATGAAC	1479
Qy	210	SerLeuProProProLysAlaProSerProProArgGlnProProProProPro	229
Db	1480	GGGATG-----ATACTATCAAGCAAGACAGATTGCT	1512
Qy	230	ProProMetSerSerSerGlySerAspTyrSerAspArgProValLeuProPro	249
Db	1513	-----ATAGAACAAACTCGAGAAATGGAACTTCATTGATA-----	1551
Qy	250	ProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAla	269
Db	1552	-----GAGTTGGAAGCTGTTGTC	1569
Qy	270	ArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrVal	289
Db	1570	AAACCCACCGAAATTTCTCAATGTAAACAACTCGGACAAGGTGTTTCGGTATTGTT	1629
Qy	290	HisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer	309
Db	1630	TACAAGGGTAGATTACTTGTATGGCGCAGAAATTCGGTAAAGAGCTATCAAAAACCTCG	1689
Qy	310	GlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArg	329
Db	1690	GTTCAAGGGACGTGTGAGTTTATGAATGAGGTGAGATTGATCGCAGGCTTCAGCATATA	1749
Qy	330	HisLeuValSerLeuValGlyTyrCysIleAlaClyAlaLysArgLeuLeuValTyrGlu	349
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Qy	350	PheValProAsnAsnLeuLeuHisLeuHisLysGlyGlyArg---ProThrMet	368
Db	1810	TATTTAGAAATTTAAGCTTCGATTCCTATCTCTCGAAATAACGAGCTCTACGTTA	1869
Qy	369	GluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHis	388
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Qy	389	GluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAsp	408
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Qy	409	PheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsn	428
Db	1990	AAAAATATGACACCAAGATCTCGGATTTTGGGATGGCCGAATCTTTTGCAAGGACGAG	2049
Qy	429	ThrHisValSerThrArg---ValMetGlyThrPheGlyTyrLeuAlaLapProGluTyrAla	447

[illegible]

Search completed: April 25, 2004, 01:02:38  
Job time : 181 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 25, 2004, 00:01:06 ; Search time 638 Seconds  
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Title: US-10-086-464-2

Perfect score: 3453

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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

ALIGNMENTS

RESULT 1

US-10-086-464-1  
; Sequence 1, Application US/10086464  
; Publication No. US20020199218A1  
; GENERAL INFORMATION:  
; APPLICANT: GORING, Daphne R. et al.  
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
; FILE REFERENCE: P 25,762-A USA  
; CURRENT APPLICATION NUMBER: US/10/086,464  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 10/069,304  
; PRIOR FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: PCT/CA00/00966  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/149,466  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: US 60/159,122  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1944  
; TYPE: DNA

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3	2285.5	66.2	2451	13	US-10-424-599-95479	Sequence 95479, A
4	1870	54.2	1724	13	US-10-425-114-2326	Sequence 2326, Ap
5	1833	53.1	2880	13	US-10-425-114-33030	Sequence 33030, A
6	1833	53.1	2881	13	US-10-425-114-33031	Sequence 33031, A
7	1748.5	50.6	1902	14	US-10-086-464-10	Sequence 10, Appl
8	1748.5	50.6	1939	14	US-10-086-464-9	Sequence 9, Appli
9	1737.5	50.3	1424	13	US-10-425-114-9117	Sequence 9117, Ap
10	1687	48.9	2025	14	US-10-086-464-13	Sequence 13, Appl
11	1687	48.9	2104	14	US-10-086-464-12	Sequence 12, Appl
12	1539	44.6	2655	13	US-10-424-599-57846	Sequence 57846, A
13	1539	44.6	2655	13	US-10-425-114-7339	Sequence 7339, Ap
14	1437.5	41.6	2190	13	US-10-425-114-14127	Sequence 14127, A
15	1437	41.6	1500	13	US-10-425-114-6300	Sequence 6300, Ap
16	1437	41.6	1552	13	US-10-424-599-47702	Sequence 47702, A
17	1415.5	41.0	2196	14	US-10-086-464-7	Sequence 7, Appli
18	1415.5	41.0	2231	14	US-10-086-464-6	Sequence 6, Appli
19	1400.5	40.6	2261	14	US-10-086-464-15	Sequence 15, Appl
20	1399	40.5	2196	14	US-10-086-464-16	Sequence 16, Appl
21	1379	39.9	2508	13	US-10-425-114-25269	Sequence 25269, A
22	1335.5	38.7	1585	13	US-10-424-599-71008	Sequence 71008, A
23	1239	35.9	1588	13	US-10-425-114-35509	Sequence 35509, A
24	1238.5	35.9	1462	13	US-10-425-114-29328	Sequence 29328, A
25	1233.5	35.7	1134	13	US-10-425-114-36420	Sequence 36420, A
26	1210	35.0	1795	13	US-10-424-599-42232	Sequence 42232, A
27	1116.5	32.3	1179	13	US-10-425-114-4027	Sequence 4027, Ap
28	1116.5	32.3	1186	13	US-10-425-114-4273	Sequence 4273, Ap
29	1115.5	32.3	981	13	US-10-425-114-7549	Sequence 7549, Ap
30	921	26.7	729	13	US-10-425-114-12191	Sequence 12191, A
31	892.5	25.8	760	13	US-10-425-114-12314	Sequence 12314, A
32	866.5	25.1	951	13	US-10-425-114-1922	Sequence 1922, Ap
33	860.5	24.9	1777	13	US-10-425-114-24475	Sequence 24475, A
34	859.5	24.9	1817	13	US-10-425-114-30665	Sequence 30665, A
35	840	24.3	2025	13	US-10-425-114-3666	Sequence 3666, Ap
36	838.5	24.3	3148	16	US-10-260-238-465	Sequence 465, App
37	837	24.2	2284	13	US-10-425-114-3455	Sequence 3455, Ap
38	825	23.9	2012	13	US-10-424-599-29210	Sequence 29210, A
39	819.5	23.7	1011	13	US-10-425-114-13131	Sequence 13131, A
40	816.5	23.6	2124	9	US-09-938-842A-1079	Sequence 1079, Ap
41	816.5	23.6	2124	11	US-09-938-842A-1079	Sequence 1079, Ap
42	811	23.5	3453	15	US-10-259-165-311	Sequence 311, App
43	806.5	23.4	2063	13	US-10-424-599-25617	Sequence 25617, A
44	804	23.3	2374	13	US-10-425-114-33063	Sequence 33063, A
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; NAME/KEY: CDS
; LOCATION: (1)..(1944)
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Score: 3453.00 Matches: 647
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Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB 1 ATGTCCTCGGCGCGCTCTCCGGGAGTGGTTCGGCTCCATCTCCACCATCAAACTCCACA 60
QY 21 ThrThrThrProProAlaSerAlaProProProThrThrProSerSerProProPro 40
DB 61 ACCACCACTCTCTCCAGCTTCGCTCTCTCCACCAACACCTCTCTCTCTCTCTCTCT 120
QY 41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
DB 121 CCATCCACTATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 61 ProSerProProThrProSerThrProGlySerProProProProProProGlnProSerPro 80
DB 181 CCATCTCCACCAACTCCATCTACGCGGGGATCTCCACCTCTCTCTCTCTCTCTCTCTCT 240
QY 81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
DB 241 CCGCTCCAACTACCGCGGATCTCCACCGCACCTGTACTCTCTCTCTCTCTCTCTCTCT 300
QY 101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
DB 301 CCACCTTCAGTCCAGGACCACTCCATCTCTCCGCGAGAGGATCTCTCTCGACCT 360
QY 121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
DB 361 CCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysteLeuLeuCys 160
DB 421 GGAAATCGCCATCGGAGGAGTCGCTCTCTGTGTGATGAGTACTCTGATTGTCTCTCTCT 480
QY 161 LysLysLysArgArgAspGluGluAspAlaTyrTyrValProProProProProProPro 180
DB 481 AAGAGAAACGACGAGAGAGACGAGAGATGCTTACTATGTTCTCTCGCCACCTCTCTCT 540
QY 181 GlyProLysAlaGlyGlyProTyrGlyGlnGlnGlnGlnThrArgGlnGlnAsnAla 200
DB 541 GGTCCCAAAAGCCGAGGACTTACGCTGACAGCAGCAACAATGGCGGCAACAAACGCA 600
QY 201 ThrProProSerAspHisValValThrSerLeuProProProProProProProProPro 220
DB 601 ACACCACTCTCAGATCATGTCGTGACGTCACCTACCACCACTCAAGGCTCTCATCTCCA 660
QY 221 ProArgGlnProProProProProProProProPheMetSerSerGlyGlySerAsp 240
DB 661 CCACGGCAACTCTCTCCACTCCACCGCTTTTCATGAGCAGGCGGCGGCTCCGAC 720
QY 241 TyrSerAspArgProValLeuProProProProProProGlyLeuValLeuGlyPheSerLys 260
DB 721 TACTCGGACCGTCCAGTCTCTCTCCACGCTCTCCAGGCTTGTGTAGGCTTCTCCAAA 780
QY 261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
DB 781 AGCACTTTCCATATCAGAGGAGCTAGTAGAGCCACCAATGGTTTCTCCGAGCGCACTTG 840
QY 281 LeuGlyGlnGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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DB 841 TTAGGACAAAGCGGTTTCGGTTACGTGCACAAAGTGTTGTTGCTTAGTGGGAAAGAGTT 900
QY 301 AlaValLysGlnLeuLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
DB 901 GCTGTGAAGACAGTTCAAAGTTGGGAGTGGTTCAGGAGAGAGGGAGTTTCAGCAGAGGTT 960
QY 321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
DB 961 GAGATCATCAGCAGAGTTCCACACAGCATCTGGTGCTCTCTTGTGGTTATTCATCGCC 1020
QY 341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
DB 1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTGTTCTTAACAACAATCTCGAGCTTCACCTC 1080
QY 361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
DB 1081 CATGCGAGGACGCGCTTACAATGGAATGGAGCACCAAGATTGAAGATTGCTCTTCGATCT 1140
QY 381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
DB 1141 GCTAAAGACCTTCTTATCTTCATGAAGATTGCAATCTCTAAATCATTCACCGTATATC 1200
QY 401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
DB 1201 AAGGCTTCAAAACATATTGATAGATTTCAGATTTCAGGCTAAGGTTGCTGATTTCGCTCT 1260
QY 421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
DB 1261 GCTAAGATTGCTTCTGATACAAACACGCAATGATCAACACGCTGTGATGGGAACCTTTGG 1320
QY 441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
DB 1321 TACTTGGCTCCGGATATACGCTGCAAGCGGAAAGCTCACGGAGAGTCTGACGTTTCTCA 1380
QY 461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
DB 1381 TTTGGCGTTGTGCTTTTGGAGCTCAATTACTGACGCTCGACCGCTTGATGCCAACATGTC 1440
QY 481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
DB 1441 TATGTAGATGACAGCTTTAGTTGACTGGGCAACGACATTTGCTTTAACCGAGACTCTGAGCA 1500
QY 501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluMet 520
DB 1501 GGAGACTTTGAGGCTTTAGCTGATCCAAAGATGAATATGGGTATGACAGAGAGATG 1560
QY 521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgProArg 540
DB 1561 GCTCGCATGTTGCTTGTGCTCGGCTTGTCTTCGCCATTTCAGCTCGCGCGAGACTCGC 1620
QY 541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
DB 1621 ATGAGCCAGATTGTGCGTGGCTTAGAAGAAATGATCACTGTGAGATCTTAAACGAAGG 1680
QY 561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
DB 1681 ATGAGACCAAGTCAAGCAATGTATACAGCTCATACGGAGGAGCACCAGATTATGACTCG 1740
QY 581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
DB 1741 AGCCAGTCAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGAAGACTCAAGAGTAC 1800
QY 601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
DB 1801 AACGCCACCGGTGAGTACAGTAATCCGACCACTAGTACTATGAGACTTACCCGCTCGTTCA 1860
QY 621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
DB 1861 AGCAGCGAGGCGCAACCCACACGCGAATGGAGATGGGGAAGATTAAAGAGAACCGGTCTAG 1920
QY 641 GlyTyrSerGlyProSerLeu 647
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Db 1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 2

US-10-086-464-3

; Sequence 3, Application US/10086464

; Publication No. US20020199218A1

; GENERAL INFORMATION:

; APPLICANT: GORING, Daphne R. et al.

; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

; FILE REFERENCE: P 25,762-A USA

; CURRENT APPLICATION NUMBER: US/10/086,464

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 10/069,304

; PRIOR FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: PCT/CA00/00966

; PRIOR FILING DATE: 2000-08-18

; PRIOR APPLICATION NUMBER: US 60/149,466

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: US 60/159,122

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2189

; TYPE: DNA

; ORGANISM: Brassica napus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2189)

; OTHER INFORMATION:

US-10-086-464-3

Alignment Scores:

Pred. No.:	1.02e-215	Length:	2189
Score:	3453.00	Matches:	647
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-086-464-2 (1-647) x US-10-086-464-3 (1-2189)

Qy 1 MetSerSerAlaProSerProGlyThrGlySerProProSerProSerProSerProSerProSerThr 20

Db 97 ATGTCCTCGCGCGCTCCGGGACCTGGTTCGCTCCATCCATCCACCACTCCACA 156

Qy 21 ThrThrThrProProAlaSerAlaProProProThrThrProSerProProPro 40

Db 157 ACCACCACTCTCTCCAGCTTCGCTCCTCCTCCACCACTCTCTCTCTCTCCCGCG 216

Qy 41 ProSerThrileProThrSerProProSerSerArgSerThrProSerAlaProPro 60

Db 217 CCATCCACTATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276

Qy 61 ProSerProProThrProSerThrProGlySerProProProProProProProProPro 80

Db 277 CCATCTCCACCACTCCATCTACCGCGGATCTCCACCTCTCTCTCTCTCTCTCTCTCT 336

Qy 81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrProThrPro 100

Db 337 CCCGCTCCACTACCGCGGATCTCCACCGGATCTCTCTCTCTCTCTCTCTCTCTCTCT 396

Qy 101 ProProSerValProGlyProProSerProSerProSerProSerProSerProSerPro 120

Db 397 CCACCTTCAGTCCCGGACCACTCCCAATCTCTCCGCGGAGGATCTCTCTCTCTCTCT 456

Qy 121 ProSerSerProSerProProSerProSerSerSerSerSerSerSerSerSerSerSer 140

Db 457 CCATCT 516

Qy 141 GlyIleAlaIleGlyGlyValAlaAlaLeuLeuValIleValThrIleIleCysLeuLeuCys 160

Db 517 GGAATGCCATCGGAGGAGTCTCTCTCTGTGTAGTGTGACTCTGTATTTGTCTCTCTGT 576

Qy 161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProProPro 180

Db 577 AAGAAGAAACGACGGAGAGAGAGATGCTTACTATGTCTCTCGCCACCTCTCTCTCT 636

Qy 181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnTyrArgGlnGlnAsnAla 200

Db 637 GGTCCCAAAACCGGAGGACCTTACCGTGGACAGCAACAATGGCGGCAACAAAGCGA 696

Qy 201 ThrProProSerAspHisValThrSerLeuProProProProProProProProProPro 220

Db 697 ACACCAACCGTCAGATCATGTGTCGTCATACCAACCAACCAACCAACCAACCAACCA 756

Qy 221 ProArgGlnProProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240

Db 757 CCACGGCAACCTCTCTCCACCTCCACCAACCAACCAACCAACCAACCAACCAACCAAC 816

Qy 241 TyrSerAspArgProValLeuProProProProProProProProGlyLeuValLeuGlyPheSerLys 260

Db 817 TACTCGGACCGTCCAGTTCTTCTCCACCGTCTCCAGGGCTTGTGTAGGCTTCTCCAAA 876

Qy 261 SerThrPheThrTyrGluGluLeuAlaAlaThrAsnGlyPheSerGluAlaAsnLeu 280

Db 877 AGCACTTTACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAATTG 936

Qy 281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300

Db 937 TTAGGACAAAGCGGCTTCGGTTACGTGCACAAAGGTGTGTTCCTAGTGGGAAAGAGTT 996

Qy 301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320

Db 997 GCTGTGAAGCAGTTGAAAGTTGGAGTGGTTCAGGAGAGAGGGAGTTTCAGGAGAGGTT 1056

Qy 321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340

Db 1057 GAGATCATCAGCAGAGTTTCACCAACGACATCTGGTGTCTCTGTGTGTATTGTCATCGCC 1116

Qy 341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360

Db 1117 GGTGCCAAAAGATTGCTTGTCTATGATTGTTCCTAACCAACATCTCGAGCTTCACCTC 1176

Qy 361 HisGlyGluGlyArgProThrMetGluTyrSerThrArgLeuLysIleAlaLeuGlySer 380

Db 1177 CATGGCAGGAGCGGCTTCAATGGAATGGAGACCCAGATTGGAAGATTGCTCTTGGATCT 1236

Qy 381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400

Db 1237 GCTAAAGACCTTCTTATCTTCATGAAGATTGCATCTTAAATCATTCACCGTGATATC 1296

Qy 401 LysAlaSerAsnIleLeuIleAspPheGlyGluAlaLysValAlaAspPheGlyLeu 420

Db 1297 AAGGCTTCAAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTGCTGTATTTGGTCTT 1356

Qy 421 AlaIlyIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440

Db 1357 GCTAAGATTGCTTCTGTATACAAACACGATGTATCAACACGCTGTGTGTGGGAACTTTGGG 1416

Qy 441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460

Db 1417 TACTTGGCTCCGGAATACGCTGCAGCGGAAAGCTCACGGAGAAGTCTGAGCTTTTCTCA 1476

Qy 461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnVal 480

Db 1477 TTTGGCGTTTGTCTTTTGGAGCTCATTTACTGGACGCTCGACCGTGTGTATGCCAACATGTC 1536

Qy 481 TyrValAspAspSerLeuValAspTyrAlaArgProLeuLeuAsnArgAlaSerGluGln 500

Db 1537 TATGTAGATGACAGCTTAGTTGACTGGGCGACGACCATTTGCTTAAACCGAGCATCTGAGCAA 1596

Qy 501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluMet 520

Db 1597 GGAGACTTTGAGGGTTTGTGTTGATGCAAAAGATGATGATGATGATGATGATGATGATG 1656

QY 521 AlaArgMetValAlaCysAlaAlaCysValArgHisSerAlaArgArgProArg 540  
Db 1657 GCTCGCATGGTGTGCTGCGGCTGTGTTCGCCATTAGCTCGCGCAGACCTCGC 1716  
QY 541 MetSerGlnIleValArgAlaLeuGluGlyAenValSerLeuSerAspLeuAsnGluGly 560  
Db 1717 ATGAGCCAGATTGCTGCTGCGTTAGAAAGAAATGTATCACTGTCAATCTTAAACGAAGG 1776  
QY 561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlySerThrAspTyrAspSer 580  
Db 1777 ATGAGACCAAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCATTATACATCG 1836  
QY 581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600  
Db 1837 AGCCAGTACAAATGAAGACATGAAGAAGTTTAGGAAATGGCACTTGGAACTCAAGAGTAC 1896  
QY 601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620  
Db 1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGAATGAGACTATGAGACTGTACCCGCTCTGGTTCA 1956  
QY 621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640  
Db 1957 AGCAGCGAGGGCCAAACACACACGGAATGGAGATGGGGAAGATTAAAGAAACCGGTGAG 2016  
QY 641 GlyTyrSerGlyProSerLeu 647  
Db 2017 GGTATAGTGGACCTTCCTT 2037

## RESULT 3

US-10-424-599-95479  
; Sequence 95479, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 95479  
; LENGTH: 2451  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_57229C.1  
US-10-424-599-95479

Alignment Scores:  
Pred. No.: 9e-140 Length: 2451  
Score: 2285.50 Matches: 450  
Percent Similarity: 80.86% Conservative: 74  
Best Local Similarity: 69.44% Mismatches: 97  
Query Match: 66.19% Indels: 27  
DB: 13 Gaps: 16

US-10-086-464-2 (1-647) x US-10-424-599-95479 (1-2451)

QY 13 ProSerProSerAsnSerThrThrThrThrProProAla-----SerAlaPro 30  
Db 246 CCCCTCCCTCCGCT---GCACTCCGTCGTACCTCCGCGGCAACTCCGTCGTCTCT 302  
QY 31 ProProThrThrProSerSerProProProProSerThrIleProThrSerProPro 50  
Db 303 CCGCGCGGACACCTCTCTCGCACCTCG-----TCAACTCCCTCTCTCGCCCCCTCG 356  
QY 51 SerSerArgSerThrProSerAlaProProProSerProProThrProSerThrProGly 70  
Db 357 -----GCGACTCCCTCCGCTTCTCCACCGTCCACTCTCTCTCTCTCCACCG 407

QY 71 SerProProLeuProGlnProSerProProAlaProThrThrThrProGlySerProPro 90  
Db 408 TCCACTCCAAACCCGCGCTCAACTTCGCGCCATCG---ACTTCTCCGCGCTCGCGGCA 464  
QY 91 -----AlaProValThrProProThrArgAsnProProProSerValProGlyProPro 108  
Db 465 TCGCACTCGCGCGCTCCGCTCCAGTGGCGCGGAGCGGAGCGGAGTCCGAGTCCACCG 524  
QY 109 SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSer 128  
Db 525 TCCCGAGCTCGCCCTCTCCCGTCGGATCGAGCCAGCACCTCCGTCGCTCCGTCG 584  
QY 129 ProSerSerAspGlyLeuSerThrGlyValValGlyIleAlaIleGlyGlyValAla 148  
Db 595 TCTTCTCTGTCAGATATTTCGACCGTGTGTGGTGGATCGCGTGGGGCTGTGGCG 644  
QY 149 LeuLeuValIleValThrLeuLysCysLeuLeuCys---LysLysLysArgArgArgAsp 167  
Db 645 GTTCTTCTTGTGTGAGCATTTCTCTGCATATGTTGCCGGAAGAGAGAGAGAGAGAGTGTAT 704  
QY 168 GluGluAspAlaTyrTyrValProProProProProProProProProProProPro 186  
Db 705 GAAGAG-----TACTATGCTCCGCGCGCGCAACCGCGCGGAGACCTAAA---GATGAT 755  
QY 187 ProTyrGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHis 206  
Db 756 GCATATGTTGTGCTCCCGCCACGTCATGG--CAACACAATGTTCCCGCTCCTCAAGATCAT 812  
QY 207 ValValThrSerLeuProPro-----ProProLysAlaProSerProProArgGln 223  
Db 813 GTGGTCTCAATGATGCTCCAAAGCCATCGCCACCATCTGCTCCACCGCTTATCTCGT 872  
QY 224 ProProProProProProPheMetSerSerSerGly-----GlySerAspTyr 241  
Db 873 CAACCTCCCGCCACCGCTCTCTTCAATGAGCAGCATGGCGGATCTGGATCAAACTAT 932  
QY 242 SerAspArgProValLeuProProSerProGlyLeuValLeuGlyPheSerLysSer 261  
Db 933 TCAGCGGTGAATTTCTTCT 992  
QY 262 ThrPheThrThrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 281  
Db 993 ACATTCAGTATGAGGAGTGGCAGCGCAACTGATGCTCTCTCTGATGCCAACCTCTCT 1052  
QY 282 GlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAla 301  
Db 1053 GGACAAAGAGGATTTGGATATGTGCACAGAGANTCTTCCCAACGGCAGAGAGTGGCA 1112  
QY 302 ValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGlu 321  
Db 1113 GTGAAGCAATTTGAAGCTGGAAGCGGCAAGGGAGCGTGAATTCGAAGTGAAGTGAAG 1172  
QY 322 IleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGly 341  
Db 1173 ATAATTAGCGGTGCTCATCAAGCATCTGTCTTCTTGGTGGATCTGCACTACATCGG 1232  
QY 342 AlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis 361  
Db 1233 TCCAGAGGCTGCTGTTTATGAATTTGTTCCCAACAACACATTTGAATTCATTTGAT 1292  
QY 362 GlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381  
Db 1293 GGAAGAGGCGACCTACCATGATGGGCCCAAGACTAAGAAATTTGCTTTAGGATCTGCT 1352  
QY 382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401  
Db 1353 AAGGAGCTGGCGTATCTTCAAGATTTGTCTCTAAGATCATCTCATGATGATATCAAA 1412  
QY 402 AlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421  
Db 1413 GCTGCAACATCTCTCGATTTTAAGTTTGAAGCAAGGTTGAGATTTTGTCTTGTGA 1472  
QY 422 LysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyr 441



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Db 1473 AAGTTTCTTCTGATGTCAATACCATGTTCTACTCGAGTGTGGGACATTTTGGGTAT 1532
Qy 442 LeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPhe 461
Db 1533 TTGGCTCCAGATATGCTTCTAGTGGAAACATGACAGACAATCAGATGTTTCTCTAT 1592
Qy 462 GlyValValLeuLeuGluLeuLeuThrGlyArgArgProValAspAlaAsnValTyr 481
Db 1593 GGAGTCTGCTCTCGAGTTAATAACCGACGACGCGCAGTCGATATAAAATCAAACTTTC 1652
Qy 482 ValAspSerLeuValAspTyrAlaArgProLeuLeuAsnArgAlaSerGluGlnGly 501
Db 1653 ATGAGGATAGTTTGGTAGACTGGCTAGGCTTGTCTCACACGAGCTTTGGAAGAGAT 1712
Qy 502 AspPheGluGlyLeuAlaAspAlaLysMetAsnGlyTyrAspArgGluGluMetAla 521
Db 1713 GATTTGATCTATTATGACCAAGGCTCCAGATGACTATGATCTTAATGAGATGCA 1772
Qy 522 ArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgProArgMet 541
Db 1773 CGAATGGTGGCTTCTGCTCGCGCTTGCATTCGTCGCAAGCGTCGACCAAGGATG 1832
Qy 542 SerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMet 561
Db 1833 AGCCAGGTTGTTCGCGCTCTGGAAGGAGATGCTCTCTAGCAGATCTTAACGAAGGAAT 1892
Qy 562 ArgProGlyGlnSerAsnValTyrSerTyrGlyGlySerThrAspTyrAspSerSer 581
Db 1893 AGACTGGACACAGCATATGTCAGTCTCAT---GAAAGCTCAGATTATGACACTGCA 1949
Qy 582 GlnTyrAsnGluAspMetLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsn 601
Db 1950 CAGTACAAGGAAGACATGAAAGTTTCAGAAATGTCATTTGGCAATCTCAGGAGTATGGT 2009
Qy 602 AlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSer 621
Db 2010 GCAAGCAGTGTAGTACAGTCCGCTACAGTGTGATGTTTAAACCCATCAGGCTCAAGT 2069
Qy 622 SerGluGly-----GlnThrArgGluMetGluMetGlyLysIleLysArgThr 638
Db 2070 AGTGAAGCAGACAGCCGCCAACCAAGGGAATGGGAATGGAATGAGAAGATGAAG---AAC 2126
Qy 639 GlyGlnGlyTyrSerGlyProSer 646
Db 2127 AATCAAGGTTTCAGTGGAGTTCT 2150

RESULT 4
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326
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Alignment Scores:

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Pred. No.: 6.61e-113 Length: 1724
Score: 1870.00 Matches: 363
Percent Similarity: 79.85% Conservative: 53
Best Local Similarity: 69.67% Mismatches: 87
Query Match: 54.16% Indels: 18
DB: 13 Gaps: 9

US-10-086-464-2 (1-647) x US-10-425-114-2326 (1-1724)
Qy 139 ValValGlyIleAlaIleGlyGlyValAlaLeuValIleValThrLeuIleCysLeu 158
Db 1 GTGCTGGCGCTGGCGCTGGCGGCTCGTGTGCTGTGCTCGCCAGCTTCATCTGCTC 60
Qy 159 LeuCys-----LysLysLysArgArgAspGluAspAlaTyrTyrValProPro 176
Db 61 TGCTGTCTCGCAAGAACGCGCGCGCGCGCGCTCAGCACTACGATACCG 120
Qy 177 ProProProProGlyProLysAlaGlyGlyProTyrGlyGlnGlnGlnGlnTyrArg 196
Db 121 CCGCCCCCGCG---CCGTACAAGAGGATCCATACGTTGGACGTACCAAGATTGG--- 174
Qy 197 GlnGlnAsnAla-----ThrProProSerAspHisValValThrSerLeuPro---Pro 213
Db 175 CAGCAAAATGGGCTCTGCTCCACCCCTGAACATGTGTCAAGATGCACCTTCGGCT 234
Qy 214 ProProLysAlaProProProProArgGlnProProProProProProProPheMet 233
Db 235 CCGCAGCATATGCAATCTCTCCACGCGCGCGCGCCACCCACCGCGATGCTA 294
Qy 234 SerSerSerGly-----GlySerAspTyrSerAspArgProValLeuProProProSer 251
Db 295 AATAGTAGTGTGGATCTGCTCTTAATTAATCTGTGTGGCGGAGATCTTACCTCCACCA 354
Qy 252 ProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAla 271
Db 355 CTTGGTCTGTTCTTGGCTTCTCGAAGAGCACATTCACCTACGAAAGAGTTGTTGAGG 414
Qy 272 ThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLys 291
Db 415 ACTGATGGATTCGGATGTCTCTCTTGGACAGGTGTTTGGCTATGTTTGCACAGA 474
Qy 292 GlyValLeuProSerGlyLysGluValAlaValLysGlnLysValGlySerGlyGln 311
Db 475 GGATTTGCTCTAATGGCAAGAGATGCTGTGTAAACAACTGGAAGTGGGCGAG 534
Qy 312 GlyGluArgGluPheGlnAlaGluValGluIleSerArgValHisHisArgHisLeu 331
Db 535 GCGAGGCTGAGTTCAGGCTGAGTTGAGATTATCAGCCGAGTACATCACAACACCTT 594
Qy 332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351
Db 595 GTGCTTTTGGTGGCTATTGCTATTCCTGAGGCAAGAGGCTGCTTGTCTATGAGTTTGC 654
Qy 352 ProAsnAsnLeuLeuGluLeuHisLeuHisGlyGluArgProThrMetGluTyrSer 371
Db 655 CCAATAAACATTTGGAAATTCACATTATACGCGAAGATCGACCAACAATGAGTGGCCT 714
Qy 372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391
Db 715 GCTAGATTAAGATCAGTTTGGGTGCTGCGCAAGGTTTACCTATCTTCTCATGAAGCTGC 774
Qy 392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411
Db 775 CATCCAAGATCATCCATCGTGACATAAAGGCATCTAACATTTCTTCTGACTTCCAATTT 834
Qy 412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisVal 431
Db 835 GAAGCTAAGGTTGCTGATTTTGGACTTTGCAAGGTTTCACTACTATAACAACACCATGTT 894
Qy 432 SerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLys 451
Db 895 TCGACAAGATTAATGGGCACCTTTGGGTATTTGGCACCTGAGTATGATCTTCTTGGCAAG 954
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QY 452 LeuThrGluLeuSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGly 471
Db CTAACAGAAAATCTGATGTAATTTTCCTTCGGAGTCATGCTTCTTGAGCTTATTACTGGG 1014
QY 472 ArgArgProValAspAlaAsnValTyrValAspAspSerLeuValAspTrpAlaArg 491
Db CGCGCACCAGTTGACACAAACCATATATGATGATGATGATGATGATGATGATGATGATG 1074
QY 492 ProLeuLeuAsnArgAlaSerGluGlnGluGluGluGluGluGluGluGluGluGluGlu 511
Db CCATTACTGATCGGACGACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1134
QY 512 AsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysVal 531
Db GGAAGGACTTCAATCCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1194
QY 532 ArgHisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsn 551
Db CGCCATTCTGCACGCTCGTGGCCAGCTATGATGATGATGATGATGATGATGATGATGATG 1254
QY 552 ValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSer 571
Db GTGTCTTTGGAGGACTTAATGAAGGTGTTCGGCTTGGCCATAGCCGCTTCTTTGGGTCA 1314
QY 572 TyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetIleValPhe 591
Db TAC---AGCAGCTCCGATTACGATCTCGCCAGTACACAGGACATGAGAAGTTCAAG 1371
QY 592 LysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSer 611
Db AAGATGGCATTCACAAACAAAC-----TATACAGCAGCAGCAATACAGCGCCCAACCA 1425
QY 612 AspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGlu 631
Db GAATATGGACAGATACCGTCTGCATCAAGCAGGAGGCGCACACAGCAGGAGAGAGAG 1485
QY 632 MetGlyLysIleLysArgThrGly-----GlnGlyTyrSerGlyPro 645
Db TCGGGTGCATAGAAAGGTGCTACAGTGGTGCTACAGCTCAGGATACAGCGGAGCC 1545
QY 646 Ser 646
Db TCG TCG 1548
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## RESULT 5

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US-10-425-114-33030
; Sequence 33030, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33030
; LENGTH: 2880
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO1705B11_F11
US-10-425-114-33030
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## Alignment Scores:

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Pred. No.: 2,75e-110 Length: 2880
Score: 1833.00 Matches: 356
Percent Similarity: 79.80% Conservative: 51
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Best Local Similarity: 69.80% Mismatches: 85
Query Match: 53.08% Indels: 18
DB: 13 Gaps: 9
US-10-086-464-2 (1-647) x US-10-425-114-33030 (1-2880)
QY 150 LeuValIleValThrLeuIleCysLeuLeuCys-----LysLysLysArgArgAsp 167
Db GTGCTGCTCGCAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
QY 168 GluGluAspAlaTyrTyrValProProProProProProProProProProProProPro 187
Db CGCGCGCTCGACACTACGATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1254
QY 188 TyrGlyGlyGlnGlnGlnGlnArgGlnGlnAsnAla-----ThrProProSerAsp 205
Db TATGTTGGAAGCTACAGAGTTGG---CAGCAAAATGGCTCTGCTGCTGCTGCTGCTGCTG 1311
QY 206 HisValValThrSerLeuPro---ProProProLysAlaProSerProProArgGlnPro 224
Db CATGTGGTCAAGATGCACCCCTTCGCTCGCCAGCATATGCCAATCGTCTCCACAGCGG 1371
QY 225 ProProProProProProProPheMetSerSerSerGly-----GlySerAspTyrSer 242
Db CCAGCGCGCGCCACCCAGCGATGCTAAATAGTAGTGTGATGCTGCTGCTGCTGCTGCTG 1431
QY 243 AspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThr 262
Db GGTGCGAGATCTTACCTCCACCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1491
QY 263 PheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGly 282
Db TTCACCTACGAAGAGCTGTGTGAGGCTACTGATGATGCTGCTGATGCTGCTGCTGCTG 1551
QY 283 GlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaVal 302
Db CAAGTGTGTTTGGCTATGTTTACAGAGGATGTGCTGCCTAATGGCAAGAGATGCTGTA 1611
QY 303 LysGlnLeuLysValGlySerGlyGlnGluArgGluPheGlnAlaGluValGluIle 322
Db AAACAATTTGAACTGGGAAGTGGCCAGGAGAGCTGAGTTCAGGCTGAGGCTGAGGAT 1671
QY 323 IleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAla 342
Db ATCAGCCGAGTACATCACAAACACCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTG 1731
QY 343 LysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGly 362
Db AAGAGGCTGCTTGTCTATGAGTTTGTCCCAATAACACATTCGAATTCACCTTACATCG 1791
QY 363 GluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLys 382
Db AAAGTTCACCAACCAATGAGTGGCTGCTGATGATTAAGATCAGTTTGGTCTGCTGCAAG 1851
QY 383 GlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAla 402
Db GGTGTTAGCTTATCTTCATGAGACTGCCATCCAAAGATCATCATCGTCGACATAAGGCA 1911
QY 403 SerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLys 422
Db TCTAAACATTTCTTCTGACTTCAATTTGAAGTAAGGTGCTGCTGCTGCTGCTGCTGCTG 1971
QY 423 IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeu 442
Db TTCCTACTGATTAACAACACCCATGTTTCGACAGAGTAATGCGGACCTTTGGGTATTG 2031
QY 443 AlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGly 462
Db GCACCTGAGTATGCTCTTCTGCAAGCTAACAGAAAAATCCGATGATTTTCTCTCGGA 2091
QY 463 ValValLeuLeuLeuIleThrGlyArgArgProValAspAlaAsnValTyrVal 482
Db GTCATGCTTCTTGAGCTTATTACTGCGCGCGCGGACGAGTTTGACACAAACCCAAACAT 2151
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Qy 483 AspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
Db 2152 GATGACAGCTGGTGTGACTGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGA 2211
Qy 503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
Db 2212 TATGATGCTTTAGTGGATCTCGGCTGGGAAGGACTTTCAATCTCAATGATGATGGCAAGA 2271
Qy 523 MetValAlaCysAlaAlaLysValArgHisSerAlaArgArgProArgMetSer 542
Db 2272 ATGATAGCTGTGCAGCTGATGTGTAGCCATTCTGCACGCTGCTGCGCACGATATGAT 2331
Qy 543 GlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562
Db 2332 CAGGTGCTTGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGG 2391
Qy 563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln 582
Db 2392 CCTGGCATAGCCGCTCTTTGGGTATAC---AGCAGCTCCGATTACGATTCTGGCCAG 2448
Qy 583 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAla 602
Db 2449 TACAACGAGCAGCATGAAGATTCAAGAGATGGCAATCAACAACAC---TATACC 2502
Qy 603 ThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSer 622
Db 2503 AGCAGCCAAATACAGCGGCCCAACAGTGAATATGACAGATACCGCTGTCATCAAGCAGC 2562
Qy 623 GluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly----- 639
Db 2563 GAGGCGACACAGCAGCAGGAGATGAGTCGGTGCAATGAAGAAAGTGCGTACAGTGGT 2622
Qy 640 -----GlnGlyTyrSerGlyProSer 646
Db 2623 GGCTACAGCTCAGGATACAGCGGAGCCTCG 2652

RESULT 6
US-10-425-114-33031
; Sequence 33031, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33031
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B12_FLI
US-10-425-114-33031

Alignment Scores:
Pred. No.: 2,75e-110 Length: 2881
Score: 1833.00 Matches: 356
Percent Similarity: 79.80% Conservative: 51
Best Local Similarity: 69.80% Mismatches: 85
Query Match: 53.08% Indels: 18
DB: 13 Gaps: 9

US-10-086-464-2 (1-647) x US-10-425-114-33031 (1-2881)
Qy 150 LeuValIleValThrLeuIleCysLeuLeuCys-----LysLysLysArgArgArgAsp 167
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Db 1139 GTGCTGCTGCCAGCTTCATCTGCCTTGTCTGCTCCGCAAGAGCGCCCGCGCCGCGC 1198
Qy 168 GluGluAspAlaTyrTyrValProProProProGlyProGlyProLysAlaGlyGlyPro 187
Db 1199 CCGCGCGCTCAGCACTACCGATACCGCGCGCCCGCGCG---CCGTACAAGGAGGATCCA 1255
Qy 188 TyrGlyGlyGlnGlnGlnTrpArgGlnGlnAsnAla-----ThrProProSerAsp 205
Db 1256 TATGGTGGAAAGTACAGAGTTGG---CAGCAAAATCGCGCTCCTGCTCCACCCCTGAA 1312
Qy 206 HisValValThrSerLeuPro---ProProProLysAlaProSerProProArgGluPro 224
Db 1313 CATGTGCTCAAGATGACCCCTTCGCTCCCGCAGCATATGCCAATCGCTCTCCACAGCGC 1372
Qy 225 ProProProProProProPheMetSerSerSerGly-----GlySerAspTyrSer 242
Db 1373 CCAGCGCGCCACCAACCGCATGCTAAATAGTAGTGGTGGATCTGCTTCTTAATCTCT 1432
Qy 243 AspArgProValLeuProProProProGlyLeuValLeuGlyPheSerLysSerThr 262
Db 1433 GGTGGCGAGATCTACCTCCACCATCCCTGGTGTCTTCTTGGCTTCTCGAAGAGACA 1492
Qy 263 PheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuGly 282
Db 1493 TTCACCTACGAAGAGCTGTGAGGCTTACTGATGGATCTCGGATGCTAATCTCTTGGGA 1552
Qy 283 GlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaVal 302
Db 1553 CAAGTGGTGTGGCTATGTTTCACAGAGGATGCTGCTAATGGCAAGAGATGCTGTA 1612
Qy 303 LysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIle 322
Db 1613 AAACAATGAAGCTGGGAAGTGGCGAGAGCGTGAGTTCAGGCTGAGGTTGAGATT 1672
Qy 323 IleSerArgValHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAla 342
Db 1673 ATCAGCGAGTATCATCAACAACCTTGTGTCTTGGTGGCTATTGCTATTTCTGAGAGC 1732
Qy 343 LysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuLeuHisLeuHisGly 362
Db 1733 AAGAGCTGCTGCTGCTATGAGTTGTCCCAATAACACATTTGGAATTCACATACG 1792
Qy 363 GluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLys 382
Db 1793 AAAGTGCACCAACAATGGAGTGGCTGCTAGATTAAAGATCACTTTGGGTGCTGCCAAG 1852
Qy 383 GlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAla 402
Db 1853 GGTATTAGCTTATCTTCATGAAGACTGCTCCAAAGATCATCCATCGTACATAAAGCA 1912
Qy 403 SerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLys 422
Db 1913 TCTAACATCTTCTTGACTTCCAATTTGAAGCTTAAGTTGCTGACTTGGCTTGGCAAG 1972
Qy 423 IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeu 442
Db 1973 TTCACCTACTGATAACAACACCCATGTTTCACAAGAGTAATGGGCACCTTTGGGTATTG 2032
Qy 443 AlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGly 462
Db 2033 GCACCTGAGTATGATCTTCTGCAAGCTAACAGAAAAATCCGATGTTATTTCTCTCGGA 2092
Qy 463 ValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrVal 482
Db 2093 GTCATGCTTCTGAGCTTATTACTGGGGCGGCGACAGTTCACACACCAACATATATG 2152
Qy 483 AspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
Db 2153 GATGACAGCTTGGTGTGACTGGGCAAGGCCATTACTGATGCGAGCAGCTTGAGGATGGTGA 2212
Qy 503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
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Db 2213 TATGATGCTTTAGTGGATCTCGGCTGGGAAAGGACTTCAATCCCTAAATGAGATGGCAAGA 2272  
Qy 523 MetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgProArgMetSer 542  
Db 2273 ATGATAGCTGTGACAGCTGCATGTGACGCCATTCTGCACGCTGCTGGCCACGTAATGAGT 2332  
Qy 543 GlnIleValArgAlaLeuGluGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562  
Db 2333 CAGGTCGTTTCGGCTTCGGAGGCAATGTCTTGGAGGACCTTAATGAAGGTGTTTCGG 2392  
Qy 563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln 582  
Db 2393 CTTGGCCATAGCCGCTTCTTTGGGTCTATAC---AGCAGCTCGGATTACGATTCTGGCCAG 2449  
Qy 593 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAla 602  
Db 2450 TACAACGAGGACATGAAGAAGTTCAAGAAGATGGGCAATTCACAACAAC---TATACC 2503  
Qy 603 ThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSer 622  
Db 2504 AGCAGCCATACAGCGCCCAACCACTGATGATGACAGATACCTCTGTCATCAAGCAGC 2563  
Qy 623 GluGlyGlnThrArgGluMetGluMetGlyLysIleLysArgThrGly----- 639  
Db 2564 CAGGCGCCACCAGCAGCAGATGAGTGGGTGCAATGAAGAAGTGGCTTACAGTGGT 2623  
Qy 640 -----GlnGlyTyrSerGlyProSer 646  
Db 2624 GGCTACAGCTCAGGATACAGCGAGCCTCG 2653

## RESULT 7

US-10-086-464-10  
; Sequence 10, Application US/10086464  
; Publication No. US20020199218A1  
; GENERAL INFORMATION:  
; APPLICANT: GORING, Daphne R. et al.  
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
; FILE REFERENCE: P 25,762-A USA  
; CURRENT APPLICATION NUMBER: US/10/086,464  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 10/069,304  
; PRIOR FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: PCT/CA00/00966  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/149,466  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: US 60/159,122  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 1902  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1902)  
US-10-086-464-10

## Alignment Scores:

Pred. No.:	5,75e-105	Length:	1902
Score:	1748.50	Matches:	367
Percent Similarity:	69.67%	Conservative:	81
Best Local Similarity:	57.08%	Mismatches:	141
Query Match:	50.64%	Indels:	55
DB:	14	Gaps:	16

US-10-086-464-2 (1-647) x US-10-086-464-10 (1-1902)

Qy 3 SerAlaProSerProGlyThrGlySerProProSerProProSerProProSerThrThrThr 22  
Db 19 TCTGCTCTCCCAACAACTCCACCTCTTCTCCATCTCCACCGCTCTAATACCAATTCACCC 78

Qy 23 ThrProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42  
Db 79 ACCTCTTCTCGG-----CCGGCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAAGGA 129  
Qy 43 ThrIleProThrSerProProSerSerArgSerThrProSerAlaProProProSer 62  
Db 130 GACTCATCATCATGCCACCTCTCTGATTCACATCTCCACAGCTCCACAAGCTCTCTAAC 189  
Qy 63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82  
Db 190 CTCTCTAAT---TCTCTAATAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246  
Qy 83 ProThrThrProGlySerProAlaProValThrProThrThrArgAsnProProPro 102  
Db 247 AGAGAAATGGAGGAACAATGGTGGCAATCATATCTCCACCGTCACGGCGCTCTCTCTCT 306  
Qy 103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg-----Pro 120  
Db 307 TCT-----CCTCTCTTAGGAGTAATAGAGATATATGGTGTAGCAGATCATCGCCA 357  
Qy 121 ProSer-----SerProSerProProProProProPro-----SerSerAsp 132  
Db 358 CCAGAGACACTGGAGGCTCTCGCTCAGACAACCTCTCTCTAGCGGAGGAGCAGTGA 417  
Qy 133 Gly-----LeuSerThrGlyValValValValGlyIleAlaIleGly 145  
Db 418 GGAGGTGGAGGTGGAAAGTAATACGAATACAGCGATCATAGTTGGTATTAGTCGA 477  
Qy 146 GlyValAlaLeuLeuValIleValThrLeuLeuCysLeuLeuValLysLysLysArg 165  
Db 478 GCTGGACTTTTGGATGATCGTTCTTATTATTGTGTCTTAGACGCAAAAGAGAGAAA 537  
Qy 166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGly 185  
Db 538 -----GACTCTCTCTAC-----CCTGAACCCCATGAAGA 567  
Qy 186 GlyProTyrGlyGlyGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp 205  
Db 568 AACCAATAT-----CAATACTA-TGGAACAACAACAACAACAACAATGCTTCACAGA 617  
Qy 206 HisValValThrSerLeuProProProProLysAlaProSerProPro----- 221  
Db 618 -----TTATCCGAATTGGCACCTAAATTCAGAGCCCAAAACCAACAATCTACTGGTGG 671  
Qy 222 -----ArgGln-ProProProProProPheMetSerSerSerGly----- 237  
Db 672 TTGGGAGCGGTGGACCATCACCGCTCTCTCTCGCGGATGCCCTACAGCGGAGAGA 731  
Qy 238 -GlySerAspTyrSer-----AspArgProValLeuProProProProGlyLeuVa 255  
Db 732 TCTTCCATGTACTCAGGCCCATCAGGCCAGTTTACCTCTCTCTCTCTCTCTCTCTAGC 791  
Qy 255 LeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275  
Db 792 CCTCGATTCAACAAGACACTTTTACTTACAGAGCTTGGCGTTCGACACAGAGGGGT 851  
Qy 275 eSerGluAlaAsnLeuLeuGlyGlnGlyPheGlyTyrValHisLysGlyValLeuPr 295  
Db 852 TAGCGATCTTAACCTTTTGGGACAGGAGGATTTGGGTATGTCCATAAAGGAGTCTTCC 911  
Qy 295 oSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArg 315  
Db 912 TAGCGGAAAGAGTAGCAGTTAAGAGTTTAAAGCGGCTAGCGACACAGGAGAGAGGA 971  
Qy 315 uPheGlnAlaGluValGluIleLeuSerArgValHisIleArgHisLeuValSerLeuVa 335  
Db 972 GTTCAAGCTGAGTGCATATCATTAGCCGTGTGATCATCGGTATCTTGTTCCTTGT 1031  
Qy 335 lGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 355  
Db 1032 TGGATATTGCATAGCTGATGGACAGAGGATGTTGGTTATGAGTTTGTCTTCAACAAA 1091  
Qy 355 nLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeu 375

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Db 1092 TTTGGATATCATCTTCATGGGAAAAATCTTCCGGTAATGAGGTCTCCCATAGTTGGC 1151
Qy 375 sileAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysI1 395
Db 1152 TATCGCTTAGTCTCGGAAGGACTCGCTTACCTTCACGAAGACTGCCATCTCGGAT 1211
Qy 395 eileHisArgAspIleLysAlaSerAsnIleLeuLeuAspPheLysPheGluAlaLysVa 415
Db 1212 CATTCACCGCGACATCAAGTCTGCAAAATATTTCTCTGGACTTCAACTTTGATGCTATGGT 1271
Qy 415 lAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVa 435
Db 1272 GGCTGATTTGGATTAGTAACTAAGTTAACTCTGATAACAACTCATGTATCTACTCGTGT 1331
Qy 435 lMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLy 455
Db 1332 GATCGGAACCTTCGGATATCTAGCTCCAGATATGCTTCAAGCGGTAAATTAACCGAAG 1391
Qy 455 sSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgProVa 475
Db 1392 ATCCGATGTTTTCTCTTACCGAGTTATGTTATTTGGAACCTTATACTGGAACACGACGGT 1451
Qy 475 lAspAlaAsnValTyrValAspAspSerLeuValAspTyrAlaArgProLeuLeuAs 495
Db 1452 TGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGCTCGGCTCTTATGGC 1508
Qy 495 nAtqAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTy 515
Db 1509 TCGCGCGCTAGAAATGGAACCTTTAATGAGCTCGCAGATCGGAGGCTTGAAGGCCAATA 1568
Qy 515 rAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysValArgHisSerAl 535
Db 1569 CAACCCGCAAGAAATGGCTCGAATGGTGACTTGTGCGGCTGCTAGCATTCGTCATTCGGG 1628
Qy 535 aAtqArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSe 555
Db 1629 GCGTAAACGCTCAAGATGAGCCAGATAGTAGTAAGCGCTTAGAAGGAAGATGTCCTTAGA 1688
Qy 555 rAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySe 575
Db 1689 TGCTTTAAACGAAGGTGGAAGCAGGACACACAGTAACTGTTACCGGTCTATGGAGCAG 1748
Qy 575 rThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLe 595
Db 1749 CTCGGATTATAGTCAGACATCTTACAATTCAGACATCAAGAAATTCAGACAGATAGCTTT 1808
Qy 595 uGlyThrGluGluTyr-----AsnAlaThrGlyGluTyrSerAsnProThrSerAs 612
Db 1809 GTCAGGCCAAGAAATTCACAGTCAGTACTGTGAAGGAACATCTTAGTAATGATTCTAGAGA 1868
Qy 612 pTyrGly 614
Db 1869 TATGGGA 1875

RESULT 8
US-10-086-464-9
; Sequence 9, Application US/10086464
; Publication No. US20020195218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
```

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1939
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-086-464-9

Alignment Scores:
Pred. No.: 5,86e-105 Length: 1939
Score: 1748.50 Matches: 367
Percent Similarity: 69.67% Conservative: 81
Best Local Similarity: 57.08% Mismatches: 141
Query Match: 50.64% Indels: 55
DB: 14 Gaps: 16

US-10-086-464-2 (1-647) x US-10-086-464-9 (1-1939)

Qy 3 SerAlaProSerProGlyThrGlySerProSerProSerProSerAsnSerThrThrThr 22
Db 36 TCTGCTCTCCAAACAAACTCCACCTCTCTCCATCTCCACCGTCTAATACCAATTCAACC 95
Qy 23 ThrProProAlaSerAlaProProThrThrThrProSerSerProProProSer 42
Db 96 ACTCTTCTCCG-----CGGCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAAGGA 146
Qy 43 ThrIleProThrSerProProSerSerArgSerThrProSerAlaProProProSer 62
Db 147 GACTCATCATCATCGCCACCTCTCTGATTCCACATCTCCACGCTCCCAAGCTCTCTAAC 206
Qy 63 ProProThrProSerThrProGlySerProProLeuProGlnProSerProProAla 82
Db 207 CCTCCTAAT---TCCTCTAATAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 263
Qy 83 ProThrThrProGlySerProAlaProValThrProProThrArgAsnProProPro 102
Db 264 AGAGGAATCGAGGAACAAATGTTGGCAATGATATCTCCACGTCACCGGCTCTCTCTCT 323
Qy 103 SerValProGlyProProSerAsnProSerArgGluGlySerProArg-----Pro 120
Db 324 TCT-----CCTCTCTCTAGGAGTAATGGAGATAATGGTGTAGCAGATCATCGCA 374
Qy 121 ProSer-----SerProSerProSerPro-----SerSerAsp 132
Db 375 CCAGGAGACTGGAGGCTCTCGCTCAGACACCTCTCTCTAGCGGAGGAGCAGTGA 434
Qy 133 Gly-----LeuSerThrGlyValValGlyIleAlaIleGly 145
Db 435 GGAGGTGGAGTGGAGAGAGTAATACGATACAGCGATCATAGTTGTTGTTAGTCGGA 494
Qy 146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArg 165
Db 495 GCTGGACTTTGATGATCGTTCTTATTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 554
Qy 166 ArgAspGluGluAspAlaTyrTyrValProProProProProGlyProLysAlaGly 185
Db 555 -----GACTCTCTCTCTAC-----CCTGAACCCATGAAAGGA 584
Qy 186 GlyProTyrGlyGlnGlnGlnGlnTyrArgGlnGlnAlaThrProProSerAsp 205
Db 585 AACCAATAT-----CAATACTA-TGGAACACACACACACAACTGCTTCACGAA 634
Qy 206 HisValValThrSerLeuProProProProLysAlaProSerProPro----- 221
Db 635 -----TTATCCGAATTGGCACCTAAATTCACAAGGCCAAACCAACAATCTACTGTGG 688
Qy 222 -----ArgGln-ProProProProProPheMetSerSerSerGly----- 237
Db 689 TTGGGAGGCGGTGGACCATCACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 748
Qy 238 -GlySerAspTyrSer-----AspArgProValLeuProProProGlyLeuVa 255
Db 749 TTCTTTCATGTACTACTAGGCCCATCACGCCAGTTTACCTCTCTCTCTCTCTCTCTCTAGC 808
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QY 255 lLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275
Db 809 CctCGaATTCaAAAGAGCATTACTTACCAAGAGCTTGGCGTGCACACAGGAGGT 868
QY 275 eSerGluAlaAsnLeuLeuGlyGlnGlyPheGlyTyrValHisLysLysGlyValLeuPr 295
Db 869 TACGGATGCTAACCTTTTGGGACAGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCC 928
QY 295 oSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgL 315
Db 929 TAGCGGAAAGAGTAGCAGATTAAAGCTTTAAAGCGGTAGCGACCAAGGAGAGAGGA 988
QY 315 uPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuVa 335
Db 989 GTTTCAGCTGAGGTGCGATATCATTTAGCGGTGTCATCATCGGTATCTTGTTCCTTGGT 1048
QY 335 lGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAs 355
Db 1049 TGGATATTGCATAGCTGATGGACAGAGGATGTGGTTTATGAGTTTGTTCCTAACAAAC 1108
QY 355 nLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTyrSerThrArgLeuLy 375
Db 1109 TTTGGAATATATCTTCATGGGAAATACTTCCGGTAATGGAGTTCTCCACTAGGTTCGG 1168
QY 375 sIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIl 395
Db 1169 TATCGCTTAGGTGCTCGGNAAGGACTCGTTACCTTCAGAGAGACTGCCATCCTCGAT 1228
QY 395 eIleHisArgAspIleLysAlaSerAsnIleLeuIleAepPheLysPheGluAlaLysVa 415
Db 1229 CATTCACCGCAGACATCAAGTCCGAAATATTCTTTGGACTTCAACTTTTGATGCTATGT 1288
QY 415 lAlaaspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVa 435
Db 1289 GCGTGAATTTGATAGCTTAAGTTAACAATCTGATAACAACACTCATGTATCTACTCGGT 1348
QY 435 lMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLy 455
Db 1349 GATGGGAACCTTCGGATATCTAGCTCCAGAAATATGCTTCAACGGTAAATTAACCGAGNA 1408
QY 455 sSerAspValPheSerPheGlyValValLeuLeuLeuIleThrGlyArgProVa 475
Db 1409 ATCCGATGTTTCTCTTACGGAGTTATGTTTGGAACTTATAACTGGGAAACGACCGGT 1468
QY 475 lAspAlaAsnAnValTyrValAspAspSerLeuValAspTTPAlaArgProLeuLeuAs 495
Db 1469 TGAT---AATGATCATCCATGGACGACACCTTAGTAGATTGGGCTCGGCCTCTTATGGC 1525
QY 495 nArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTy 515
Db 1526 TCGCGCGCTAGAAAGATGGAAACTTTTAATCAGCTCGCAGATCGAGGCTTGAAGGCAACTA 1585
QY 515 rAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAl 535
Db 1586 CAACCGCAAGAAATGGCTCGAATGTGACTTGTGCGCTGTAGCATTCGTCAATTCGGG 1645
QY 535 aArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSe 555
Db 1646 GCGTAAACCTCAAAGATGAGCAGATAGTAGAGCGTTAGAGGAGAAAGTGTCTCTTAGA 1705
QY 555 rAspLeuAnGluGlyMetArgProGlyGlnSerAnValTyrSerSerTyrGlyLys 575
Db 1706 TCGTTTAAACGAAGGTGTGAAGCCAGGACACAGTAACGTTTACGGGTCTATTGGGAGCAAG 1765
QY 575 rThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLe 595
Db 1766 CTCGGATTATAGTCAGACATCTTACAATGCAGACATGAAGAAATTCAGACATAGCTTT 1825
QY 595 uGlyThrGlnGluTyr-----AsnAlaThrGlyGluTyrSerAsnProThrSerAs 612
Db 1826 GTCGACCAAGAAATCCCCAGTCAGTGTGGAAGNAACATCTAGTAATGATTTAGAGA 1885
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QY 612 pTyxGly 614
Db 1886 TATGGGA 1892
RESULT 9
US-10-425-114-9117
; Sequence 9117, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9117
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700833950_FLI
US-10-425-114-9117
Alignment Scores:
Pred. No.: 2,266-104 Length: 1424
Score: 1737, 50 Matches: 331
Percent Similarity: 88.73% Conservative: 47
Best Local Similarity: 77.70% Mismatches: 41
Query Match: 50.32% Indels: 7
DB: 13 Gaps: 4
US-10-086-464-2 (1-647) x US-10-425-114-9117 (1-1424)
QY 226 ProProProProProProPheMetSerSerSerGly-----GlySerAspTyrSerAsp 243
Db 12 CCCCCACCACCCGCCCTCTTTCATCAGCAGCAGTGGCGGATCTGGATCAACACCAATTCCAGC 71
QY 244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
Db 72 GGTGAATTTCTCTCTCTCTCTCTCCAGAAATTTTCATTTGGGTTCTCTAAGAGCACATTTC 131
QY 264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
Db 132 ACGTATGAGGAGTTGGCACGCGCAACTGATGGCTTCTCTGATGCCAACCTCTCTGGACAA 191
QY 284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
Db 192 GGAGATTTGGATATGTGCACAGAGAAATCTTCCACGCGCAGAGGTTGAGTGAAGTTTGAATAATT 311
QY 304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleLe 323
Db 252 CAATTTGAAGGCTGGAAGCGGCAAGGGAGCGTGAATTTCCAAAGCTGAAGTTGAGATAATT 343
QY 324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
Db 312 AGCCGTGTCCATCAACAAGCATCTTGTCTTTGGTTGGATCTGTCATCACTGGGTCGCCAG 371
QY 344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuLeuGluHisGlyGlyGlu 363
Db 372 AGGCTGCTGTGTTTATGAATTTGTTCCCAACCAACATTTGGAATTCATTTGATGGAAAA 431
QY 364 GlyArgProThrMetGluTyrSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
Db 432 GGGAGACCTACCATGATTTGGCCCAAGACTTAAGAATTTGCTTTAGGATCTCTTAAGGGA 491
QY 384 LeuSerTyrLeuHisGluAspCysAnProLysIleIleHisArgAspIleLysAlaSer 403
Db 403
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Db 492 CTGGCGTATCTTCATGAGAGATTGTCTATCCTTAAGATCATCTCGTGTATCAATCAATCTGCC 551  
Qy 404 AsnIleuIleuAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423  
Db 552 AACATCCTCTGGATTTTAAGTTTGAAGCAAGGTTGCAGATTTCGTCTTGCAAGTTT 611  
Qy 424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443  
Db 612 TCTTCTGATGTCATACCCATGTTTCTACTCGAGTCATGGGAGCTTTTGGGTATTGGCT 671  
Qy 444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463  
Db 672 CCAGATATCTTCTAGTGAAGAACTCACAGCAATCAGATGTTTCTCTATGGAATC 731  
Qy 464 ValLeuLeuGluLeuIleThrGlyArgProValAspAlaAsnValTyrValAsp 483  
Db 732 ATGCTCTCTGAGTTAATAACCGGACGAGCCAGTTGATATAAAATCAAACTTACATGGAG 791  
Qy 484 AspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPhe 503  
Db 792 GATAGTTTGGTAGATTGGGCTAGGCTTTCCTCACAGAGCTTTGGGAAGAGGATGATTTT 851  
Qy 504 GluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMet 523  
Db 852 GATCTATATATGACCCAGGCTCCAGAAATGACTATGATCCTCATGAGATGGCAGCATG 911  
Qy 524 ValAlaCysAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln 543  
Db 912 GTGGCTCTGCTGGGCTTCATACGTCATTCGGCAAGGCTGCACCAAGGATGAGCCAG 971  
Qy 544 IleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgPro 563  
Db 972 GTTGTGCGGCTCTCGAAGGAGATGTCTCTAGCAGATCTGAATGAAGGAATAAGACCT 1031  
Qy 564 GlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyr 583  
Db 1032 GGACACAGCACTATGATAGTTCTTCAT---GAAGCTCAGATTATGACATGCACAGTAC 1088  
Qy 584 AsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThr 603  
Db 1089 AAGGAAGACATGAAAGTTTCAGGAATGCGCATTCGGAACTCAGGAGTATGGTCAAGC 1148  
Qy 604 GlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerGlu 623  
Db 1149 AGTCAGTACAGTCCCGCTACAAAGTGAATGATGTTTAAACCCATCAGGCTCAAGTAGTAA 1208  
Qy 624 Gly-----GlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640  
Db 1209 GCACAGAGCGCCCAACCAAGGGAATGGAATGAGAAGATGAAG---AACAATCAA 1265  
Qy 641 GlyTyrSerGlyProSer 646  
Db 1266 GGTTTCAGTGAAGTTCT 1283

## RESULT 10

US-10-086-464-13  
; Sequence 13, Application US/10086464  
; Publication No. US20020199218A1  
; GENERAL INFORMATION:  
; APPLICANT: GORING, Daphne R. et al.  
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
; FILE REFERENCE: P 25,762-A USA  
; CURRENT APPLICATION NUMBER: US/10/086,464  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 10/069,304  
; PRIOR FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: PCT/CA00/00966  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/149,466  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: US 60/159,122  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 2025  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2025)  
US-10-086-464-13  
  
Alignment Scores:  
Pred. No.: 6,08e-101 Length: 2025  
Score: 1687.00 Matches: 368  
Percent Similarity: 63.99% Conservative: 87  
Best Local Similarity: 51.76% Mismatches: 142  
Query Match: 48.86% Indels: 114  
DB: 14 Gaps: 25

US-10-086-464-2 (1-647) x US-10-086-464-13 (1-2025)

Qy 1 MetSerSerAlaProSerProGlyThrGlySerProSerProSerProSerAsnSerThr 20  
Db 16 GTGGATTTCATCTCTGCCCTGAAACC---TCAAATGGGACACACCGTCAAACGGAACA 72  
Qy 21 ThrThrThrProProAlaSerAlaProProProThrThrProSerSerProPro 40  
Db 73 TCG-----CCGTCTAATGAGTCATCGCCGCCCAACACACCGCTTCTTCAACCAACCA 123  
Qy 41 ProSerThrIleProThrProProProSerProSerSerArgSerThrProSerAlaPro 60  
Db 124 TCATCA-----ATATCTGCTCTCCGCCAGATATCTCCGCTTCTTTTCAACCGCG 174  
Qy 61 ProSerProProThr-----ProSerThrProGlySerProProProLeu 75  
Db 175 CCGTGCACCAACGAGAAACGTCACCTCTACATCTCGTCTCATCGCCGCTGT 234  
Qy 76 -----ProGln-----ProSerProProAlaPro-----Thr 84  
Db 235 GTAGCTAATCCGTCACCGCAGACTCCAGAGAAATCTTCTCCACCTGCACCTGAAGGCTCA 294  
Qy 85 ThrProGlySerProProAla---ProValThrPro-----ProThrArgAsn 99  
Db 295 ACTCCTGTAAAGCCACCTGCACCAACCAACACCGTCGAACCAANTCACCGAAAGACCA 354  
Qy 100 ProProPro-----Pro----- 102  
Db 355 ACTCCTCTCTCTCTGTGTGCAATGATGATCGGAAACAGAACCAATGCGGAAACCAAC 414  
Qy 103 -----SerValProGlyProProSerAsnProSerArg-----GluGlyGly 116  
Db 415 AGAGACGGCTCCACACCATCACCACCGCTCTCAGGGAACAGAACTTCCGGTGACGGTGC 474  
Qy 117 SerProArgProProSerProSerProProSerProSerSerAspGlyLeuSerThr 136  
Db 475 TCACCTTCACCACTCGTGTGATAGCCCTCTCAGAANTAGTGAGATTCAGACTCATCA 534  
Qy 137 GlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIle 156  
Db 535 TCG-----GGGCTT-----TTGCTTCTACTTGCAGTGTGATT 567  
Qy 157 CysLeuLeuCysLysLysLysArgArgAspGluGluAspAla-----Tyr 172  
Db 568 TGCATCTGTTGCAACAGGAAGAAAGAAATAATCTCTCAGGTCAACCACTGCACTAC 627  
Qy 173 TyrValProProProProProGlyProLysAla---GlyGlyProTyrGlyGln 191  
Db 628 TACAATAACAATCCTTATGGAGGAGGAGCCCTCAGGTAATGGTGTATTATCAAGGGA--- 684  
Qy 192 GlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeu 211  
Db 685 -----ACACCTCAAGATCATGTGGTG---AATATG 711  
Qy 212 ProProProProLysAlaProSerProProArgGlnProProProProProProPro 231





## US-10-424-599-57846

Alignment Scores: 3.3e-91 Length: 2655  
Pred. No.: 1539.00 Matches: 341  
Score: 55.19% Conservative: 95  
Best Local Similarity: 43.16% Mismatches: 141  
Query Match: 44.57% Indels: 213  
DB: 13 Gaps: 19

US-10-086-464-2 (1-647) x US-10-424-599-57846 (1-2655)

Qy 2 SerSerAlaProSerProGlyThrGlySerProProSerProSerAsnSer----- 19  
Db TCATCTCTCCCAACA---AACACTTCCACCCACCACTCCTCCAGTCTCTCTCAGCCT 154  
Qy 20 -----ThrThrThrProProProAlaSerAlaPro---ProProThrThr 34  
Db AATCAACAACAACAACAACAACAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 214  
Qy 35 ProSerSerProPro-----ProProSerThrThrThrSerProProProSerSer 52  
Db CTTCTGTCT 274  
Qy 53 ArgSerThrPro-----SerAlaProProProProProProProProProProPro 69  
Db TCACGTCT 334  
Qy 70 GlySerProProProPro-----GlnPro 78  
Db GATTCCTCCACCACTTGCACCTGTCATCTCCAAACCCCAACCACTTACCAACATCT 394  
Qy 79 SerProProAlaProThrProGlySerProProAlaProValThrProProThrArg 98  
Db TCACCAACCACTTGCACCTGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 454  
Qy 99 AnProProProSerValPro-----GlyProProSerProSerProSerArgGlyGly 116  
Db GAAATCCCACT 505  
Qy 117 SerProArgPro-----ProSerSerPro 124  
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Qy 125 SerProProSerProSer----- 130  
Db TCT 625  
Qy 130 ----- 130  
Db GAAATCCCAACCACT 685  
Qy 130 ----- 130  
Db CCTAAACCT 745  
Qy 130 ----- 130  
Db GACCTCTCAGGATCTTACCTCCAGTCTTTCGCTGATCCCACTTCTCTCTCTCTCTCT 805  
Qy 130 ----- 130  
Db GTGGGGGTCCGAAGTGTGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 865  
Qy 131 ----- 131  
Db ACTAATGATGGTACTAACAGTATGTCTTCAAAACAACACACCTTCTCTCTCTCTCTCT 925  
Qy 135 SerThrGly-----ValValValGlyLeuAlaLeuGlyValAlaLeuValLeu 152  
Db ACACCTGGAGGATCTGTGGCTATTTGGATTTGGATTTGGATTTGGATTTGGATTTGG 985  
Qy 153 ValThrLeuLeuCysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 172

Db GTTATGGCTGT 1045  
Qy TyrValProProProProProProProProProProProProProProProProProPro 192  
Db TATGTGTCT 1063  
Qy GlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuPro 212  
Db -----TTTACCCTCATCCCACTTCCAGTACCTTATTC 1096  
Qy 213 Pro 232  
Db TTAGGCGCCGAGTCTCCGCC-----AACCTT 1123  
Qy 233 MetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProProProProPro 252  
Db TTAGGTAGTGTCTCTGT 1171  
Qy 253 GlyLeuValLeuGlyPheSerSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272  
Db GGT 1228  
Qy 273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisGly 292  
Db AATGGT 1288  
Qy 293 ValLeuProSerGlyGlyValAlaValValValValValValValValValValVal 312  
Db TTTGT 1348  
Qy 313 GluArgGluPheGlnAlaGluValGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 332  
Db GACCGCGAATTCAGGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1408  
Qy 333 SerLeuValGlyTyrCysIleAlaGlyAlaValValValValValValValValVal 352  
Db TCTTTAGT 1468  
Qy 353 AsnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 372  
Db AACGATATCT 1528  
Qy 373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392  
Db AGAGTCAAGT 1588  
Qy 393 ProLysIleLeuHisArgAspIleLysAlaSerAsnIleLeuLeuLeuLeuLeuLeuLeu 412  
Db CCACGATATTCATCGAGATATTAAAGTCATCAACATCTCTCTCTCTCTCTCTCTCTCTCT 1648  
Qy 413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432  
Db GCTCAAGT 1708  
Qy 433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452  
Db ACACGTGTAAATGGGAACCTTTGGGTACATGGCAGCAATATGCGCAAGTGGAAACTT 1768  
Qy 453 ThrGluLysSerAspValPheSerPheGlyValValValValValValValValValVal 472  
Db ACTGAAAAAGTCTGATGTATATCTTTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1828  
Qy 473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492  
Db AGCCTGTAGATGTATCTCAACCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1888  
Qy 493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGlyGlyLeuAlaAspAlaLysMetAsn 512  
Db CTGTTGACGGAAGCACTTGACAAATGAGGACCTTTGAAATTTTGGTGTGTGTGTGTGTGT 1948  
Qy 513 AsnGlyTyrAspArgGluMetAlaArgMetValAlaCysAlaAlaCysValArg 532

Db 1949 AAGACTACGATAGAAATGTTTCCGATGATCGAGGTCGCCGAGCCTGTGTACGC 2008  
Qy 533 HiserAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552  
Db 2009 CACTCATCGGTGAAGAGACACGACGATCAGTCAGGTGTGAGAGCTTTAGATTCTCTGGAT 2068  
Qy 553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572  
Db 2069 GAGTTTACGATCTCAATAACGGAATGAACCGGACAGAGATTCCGGT----- 2116  
Qy 573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592  
Db 2117 -----TTTGATTCCGCGCAGCAATCTGCACAAATCAAGATGTTTAGAGG 2161  
Qy 593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612  
Db 2162 ATGGCTTTTGGAGCCAAAGT-----AGTTCGGTTCCTCAATGAGTCTCAGAGTAGC 2215  
Qy 613 Tyr-GlyLeuTyrProSerGlySerSerGluGlyGlnThrThrArgGluMetGluMe 632  
Db 2216 TGGAGGAGTA-----GAGATCAGCAGCCACCAACTGTCTTC 2251  
Qy 632 tGlyLysIleLysArgThrGlyGlnGly 641  
Db 2252 TCCCAATAAATA---CTGGCATGGGA 2276

## RESULT 13

US-10-425-114-7339  
; Sequence 7339, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 7339  
; LENGTH: 2655  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700652889\_FLI  
US-10-425-114-7339

Alignment Scores:  
Pred. No.: 3,3e-91 Length: 2655  
Score: 1539.00 Matches: 341  
Percent Similarity: 55.19% Conservative: 95  
Best Local Similarity: 43.16% Mismatches: 141  
Query Match: 44.57% Indels: 213  
DB: 13 Gaps: 19

US-10-086-464-2 (1-647) x US-10-425-114-7339 (1-2655)

Qy 2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSer----- 19  
Db 98 TCATCTTCTCAACA---AACACTTCCACCCGACCATCAGTCTCTCTCAGCCT 154  
Qy 20 -----ThrThrThrThrProProProAlaSerAlaPro-----ProProThrThr 34  
Db 155 AATCAAAACAAACAAACAAACAAACCAATTTCCCTGCTCTTCTCTCTCTGAC 214  
Qy 35 ProSerSerProPro-----ProProSerThrIleProThrSerProProSerSer 52  
Db 215 CCTTCTGCTCCACCT 274

Qy 53 ArgSerThrPro-----SerAlaProProProProSerProProThrProSerThrPro 69  
Db 275 TCATGTGCTCTCCACCATCATCTACACCAACCACTTTGGCCCTCCATCATCAACACCT 334  
Qy 70 GlySerProProProLeuPro-----GlnPro 78  
Db 335 GATTCTCCACCATTCGCACTGCAATCTCCAAACCCACAGTACAAACATCTCCCCC 394  
Qy 79 SerProProAlaProThrThrProGlySerProProAlaProValThrProProThrArg 98  
Db 395 TCACCAACGATTACAACATCTCCCTCCACCAACAGTACCAACATCCCTCTCCAGCT 454  
Qy 99 AsnProProProSerValPro-----GlyProProSerAsnProSerArgGluGlyGly 116  
Db 455 GAAACCTCCACCTCTCCCTTCCAAATTTGTCTCCACCATCTCCACAGCC-----GGT 505  
Qy 117 SerProArgPro-----ProSerSerPro 124  
Db 506 TCCCTCTCTCTCAATCACTCCCAACAAATTCACCTCCCTCTCGACGATTTCCGCA 565  
Qy 125 SerProProSerProSer----- 130  
Db 566 TCTCTCTCTCTCCGGCCAAATTTTCCAAAGCCCAACCACTAGAACTCTCTCCAGAGAA 625  
Qy 130 ----- 130  
Db 626 GAAAAATCCACCAAAACTACTCTCTCATGTCATCTCTCCATCAGTTTCTGAAACTCT 685  
Qy 130 ----- 130  
Db 686 CTTAAACCTCTCTCTCTGATGTTCCCTCCATCCATGCTTCAACTCTCTCTCTCTTCA 745  
Qy 130 ----- 130  
Db 746 GACCTTCAGGATCTTCACTCCAGCTTCTTGCTGATCCCTCCCAACTATAAACAACAGT 805  
Qy 130 ----- 130  
Db 806 GTGGGGGTCGGAAGGTGTCGCTACCTCTCTTCCAACCTGAGAAACCACTGTAGACCT 865  
Qy 131 -----SerAspGlyLeu 134  
Db 866 ACTAATGATGGTACTAACAGTATGTCTTCAACAAACACACTTTCACATTTCTGGAGGTTG 925  
Qy 135 SerThrGly-----ValValValGlyIleAlaIleGlyValAlaLeuLeuValIle 152  
Db 926 AGCACTGGAGGATCTGTGGCTATTGGAATTGTAGTTGTTTATTGTCTCAGCCTTCTT 985  
Qy 153 ValThrLeuIleCysLeuLeuCysLysLysLysLysLysLysLysLysLysLysLysLys 172  
Db 986 GTTATGGCTGTGTGTTTGCACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1045  
Qy 173 TyrValProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGln 192  
Db 1046 TATGCTGCTCTCTCTCA----- 1063  
Qy 193 GlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuPro 212  
Db 1064 -----TTTACCTCATCCCAATTCAGGTACCTTATTC 1096  
Qy 213 ProProProLysAlaProSerProProArgGlnProProProProProProProPhe 232  
Db 1097 TTGAGGCGGAGTCTCCGGC-----AACTTT 1123  
Qy 233 MetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerPro 252  
Db 1124 TTAGGTAGTGGCTCTGTGTAGTATTT-----GTATATTCTCATCAGAGCT 1171  
Qy 253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272  
Db 1172 GGTGGTGTA---AGTAGTTCAAGATCATGGTTCACATATGAAGAACTTATTCAAGCTACA 1228  
Qy 273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlyGlnGlyPheGlyTyrValHisLysGly 292

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Db 1229 AATGGGTTTTTCAGCACAAAATTTGTTGGAGAGGTGGATTTGGCTGTGTTTATAAAGGT 1288
Qy 293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312
Db 1289 TTGCTGATAGATGGAAGAAGTAGTACTGTGAACAGCTCAAAATTTGGTGGTGGCAAGG 1348
Qy 313 GluArgGluPheGlnAlaGluValGluLeuLeuLeuLeuLeuLeuLeuLeuVal 332
Db 1349 GAACCGGAATTCAGGCGAGAGTTGAGATTATTAGCCGTGTACATCATCGTCNCTGGTT 1408
Qy 333 SerLeuValGlyTyrCysAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
Db 1409 TCTTTAGTTGGTTACTGATATCCGAGCATCAGAGATGCTTGTATATGACTATGTTCC 1468
Qy 353 AsnAsnAsnLeuLeuLeuHisGlyGlyGluGlyArgProThrMetGluTrpSerThr 372
Db 1469 AACGATATCTCTTCAATTCATCTCCACGGTGAATAGACAGTTCTAGATTGGCCCTACC 1528
Qy 373 ArgLeuLysAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
Db 1529 AGAGTCAGAGTTGCTGCTGGTGCAGCTCGTGGATAGCTTACTTGCATGAAGACTGTGAT 1588
Qy 393 ProTyrLeuLeuHisArgAspIleLysAlaSerAsnIleLeuLeuAspPheLysPheGlu 412
Db 1589 CCACGCATTTATTCAGAGATATTAAATCATCAACATCTCTACTGTATCTCAACTATGAA 1648
Qy 413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
Db 1649 GCTCAAGTTTCGGACTTTGGGCTTCCAAATTTGGCATTTAGATTCAAAATACACATGTAAT 1708
Qy 433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
Db 1709 ACACGTGTAAATGGGAACCTTTGGGTACATGGCCACGACGAAATATCGCAAGTGGAAACTT 1768
Qy 453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuLeuThrGlyArg 472
Db 1769 ACTGAAAAGTCTGATGTATATTTCTTTGGGGTGTGCTTTTGGAGCTAATTACAGGTCGG 1828
Qy 473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
Db 1829 AAGCCTGTAGATGTCATCTCAACAAATGGTGTATGAGAGCTGGTTGAATGGGCTCGACCT 1889
Qy 493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGlyGlyLeuAlaAspAlaLysMetAsn 512
Db 1889 CTGTTTGACGGAAGCACTTGACATGAGGACITTTGAATTTTGGTGATCCAAGACTGGGG 1948
Qy 513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysValArg 532
Db 1949 AAGAACTACGATAGAAATGAAATGTTCCGATGATCGAGGCTCGCCGACGCTGTGTACGC 2008
Qy 533 HisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552
Db 2009 CACTCATCGGTGAAGAGACCACGATGAGTACGAGTGGTGGAGAGCTTTAGATCTCTGGAT 2068
Qy 553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572
Db 2069 GAGTTTACGGATCTCAATAACGGATGAACCGGACAGAGTTCGGTG----- 2116
Qy 573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592
Db 2117 -----TTTGATTCGGCGCAGCAATCTGCACAAATCAGAATGTTTAGGAGG 2161
Qy 593 MetAlaLeuGlyThrGlnCluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612
Db 2162 ATGGGCTTTGGAGGCAAGAT-----AGTTCGGTTTCTTCAATGAGTCTCAGATGAGC 2215
Qy 613 Tyr-GlyLeuTyrProSerGlySerSerGluGlyGlnThrThrArgGluMetGluMe 632
Db 2216 TGGAGGAGTA-----GAGATCACGACCCCACTGCTCTC 2251
Qy 632 tGlyLysLeuLysArgThrGlyGlnGly 641
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Db 2252 TCCAAAATAAAA---CTGGGCATGGGA 2276
RESULT 14
US-10-425-114-14127
; Sequence 14127, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14127
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-034-DS_FLI
US-10-425-114-14127
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Alignment Scores:
Pred. No.: 1,09e-84 Length: 2190
Score: 1437.50 Matches: 331
Percent Similarity: 61.90% Conservative: 80
Best Local Similarity: 49.85% Mismatches: 167
Query Match: 41.63% Indels: 87
DB: 13 Gaps: 19
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US-10-086-464-2 (1-647) x US-10-425-114-14127 (1-2190)
Qy 1 MetSerSerAlaProSerProGlyThrGlySerProPro----- 13
Db 2 ATGATGCCTTCTTCCCTCCCTCATTCCTCGCTCGCCCATTCACCTTCGACGACCCCTT 61
Qy 14 SerProProSerAsnSerThrThrThrThrThrProProAlaSerAlaProPro----- 31
Db 62 TCTCCTTCTCCTCTCTCAATCACCTGCAGCGCAAGAAAGGGGTGTGAGAGTAACTA 121
Qy 31 ----- 31
Db 122 AGAGCTATTTAGCAATAATACATACATAGTATATACCTCTTTAGGTCAAGGGTGGAGT 181
Qy 32 ---ProThrThrProSerSerProProProProSerThrIlePro----- 45
Db 182 TCTCCTTATTCGGAGGAAGAGCTCCATCCTCATCTTCTACAGACCAACCAATAAATGGCC 241
Qy 46 ThrSerProProProSerSerArgSerThrThrThrThrThrThrThrThrThrThrThr 65
Db 242 TCTAGCCACAGTCTCTCGCCATCATCTCCAAAGAGTCCGCCACCAACCAAGACATCA 301
Qy 66 ProSerThrProGlySerProProProProGlnProSerProAlaProThrThr 85
Db 302 GCTTTGGCGCCAAATCATCTTCA-----AAGTCACCTCGCCACCAAGGGTGAATCA 355
Qy 86 ProGlySerProAlaProValThrProProThrArgAsnProProProSerValPro 105
Db 356 ---AATTTCATCTCCCGAGTCCCATCGAAATCGTCTGTCACCAACCCGACCAAG 412
Qy 106 GlyProProSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSer 125
Db 413 AAAAGTGTGTACATCTAGCTCTAAAGATGGGAAGCAAGTGTCTTTCATCGTCT 472
Qy 126 ProProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGly 145
Db 473 TCATCGTCGGATATACAGCCGCTGTGATCATCCGCGGTGTGCTTGGGGTG---GTGGGC 529
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Qy 146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165  
Db 530 TTCGCTCTGCTTTGTCATCGTGGCGTGTGCTGCGCAAGAAAGAAAGAAACGT 589  
Qy 166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyPro----- 182  
Db 590 -----CCGCCCCCAATGAACATGCCCTTCTACACC 619  
Qy 183 ---LysAlaGlyGly-----ProTyrGlyGlyGlnGlnGlnGlnGlnGln 198  
Db 620 GACGAGAAAGCAATGTATTATCCCAACGCTGCTGCGCGCTATGTGGCAGCAATAT 679  
Qy 199 AsnAlaThrProProSerAspHisValThrSerLeuProProProProProLysAlaPro 218  
Db 680 GGCAGCAAC-----GGCAGCATCCCTCCGCGGG-ATGCGACCA 717  
Qy 219 SerProProArgGlnProPro-ProProProProProPheMetSerSerSerGlyGly 238  
Db 718 TCACGGCGGGGAACCGCTGTCGCATCGCTGGGTGCGATGGCGGCGCCCTGACGGG 777  
Qy 238 ySerAspTyrSerAsp-----ArgProValLeuProProProSerProGlyLeuVa 255  
Db 778 CGAGATGTAATCGTCCGCGCGCCCGGCTCCCTCCCGCCACCTTCGCGGACGTGGC 837  
Qy 255 LLeuGlyPheSerLysSerThrPheThrTyrGluLeuAlaAlaAlaThrAsnGlyPhe 275  
Db 838 GCTGGGGTTCTCAAGAGCTCTTCTGTCAGAGAGCTAGCGGAGCGACGTCCGGCTT 897  
Qy 275 eSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPr 295  
Db 898 CTCGTCGCGCACTCTGCGGCGAGGCGGTTCGGGTACGTGTACAGGCGGTGCTCGC 957  
Qy 295 o---SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluAr 314  
Db 958 CGGCAGCGGGAAGGAGGTGGCGGTGAAGCAGCTCAAGTCCGGGAGCGGCGAGGGGAGCG 1017  
Qy 314 gGluPheGlnAlaGluValGluIleLeuSerArgValHisHisLysLeuValSerLe 334  
Db 1018 CGAGTTCCAGCGGAGGTGGAGATCATCAGCGCGGTGCACCGCTCACCTGTGTGCT 1077  
Qy 334 uValGlyTyrCysteAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAs 354  
Db 1078 CGTGGGTACTGCATCGGCGCAACCGAGCGATGCTGTACGAGTTCGTGGCGCAACA 1137  
Qy 354 nAsnLeuGluLeuHisLysHisGlyGlyArgProThrMetGluTrpSerThrArgLe 374  
Db 1138 CACCTGGAGCACCATCTGTACGCCAAGAGCGGCTGTATGAGTGGAGCACCAGCAT 1197  
Qy 374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLy 394  
Db 1198 GAAGATCGCGCTCGGCTCCGCGCAAGGCGCTCGCTACCGATCTCCACGAGACTGCCATCCTCG 1257  
Qy 394 sIleIleHisArgAspIleLysAlaSerAsnIleLeuLeuAspPheLysPheGluAlaLy 414  
Db 1258 GATCATCCCGCGACATCAAGCGCGCAACATCTGCTGGCAACAACATTCGAGGGCAT 1317  
Qy 414 sValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrAr 434  
Db 1318 GGTGGCGGACTTCGGCTGGCGAGCTCAGCAGCGACCAACAGCAGCATCTCCACGGC 1377  
Qy 434 gValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGl 454  
Db 1378 CGTCATGGGCACTTCGCTACCTCGCGCGCGAGTACGCGTCCAGCGCAAGCTCAGCGA 1437  
Qy 454 uLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgPr 474  
Db 1438 CAGTCCGAGCGTCTTCTCTTCGCGGTATGCTGCTGAGCTACTCAGCGGCGCGCGCC 1497  
Qy 474 oValAlaAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLe 494  
Db 1498 CATCATACCAACCAAC---TACATGGAGGACAGCTGTGTGAGTGGGCGCGCGCTGCT 1554  
Qy 494 uAsnArg-----AlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAs 512

Db 1555 GAGCGCGCGCTCGCGGGGAGACGGGC---TTGCGCGAGCTCGTCACCCCTCTGGG 1611  
Qy 512 nAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaCysValAr 532  
Db 1612 AGCGAGTACTCGTCTCGAGGTGGAGCGCTTGGCGGCTTGGCGCGCTGGAGGCGAGC 1671  
Qy 532 gHisSerAlaArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVa 552  
Db 1672 CCATCGCGCAAGCGCGCCCAAGATGAGCCAGATCGTGGCGCGCTGGAGGCGAGCG 1731  
Qy 552 lSerLeuSerAspLeuAsn---GluGlyMetArgProGlyGlnSerAsnValTyrSerSe 571  
Db 1732 ATCGCTCGAGGATCTGCACGAGCGCGCAAGCGCGGAGCGCTCTCTCTCTCC-- 1789  
Qy 571 rTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheAr 591  
Db 1790 ---GGCGGTGGCTCCGAC-----AACATCTCCCGCTTAAG 1821  
Qy 591 gLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGlyTyrSerAsnProThrSe 611  
Db 1822 GCAGTCGCTTCGACAGCGCGACTACTCG-----GACTACAGCAGCAGCTCCTC 1872  
Qy 611 rAspTyrGly 614  
Db 1873 CACCGTGGT 1882  
RESULT 15  
US-10-425-114-6300  
; Sequence 6300, Application US/10425114  
; Publication No. US20040034889A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 6300  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700560157\_FLI  
US-10-425-114-6300  
Alignment Scores:  
Pred. No.: 8.16e-85 Length: 1500  
Score: 1437.00 Matches: 284  
Percent Similarity: 74.27% Conservative: 45  
Best Local Similarity: 64.11% Mismatches: 80  
Query Match: 41.62% Indels: 34  
DB: 13 Gaps: 7  
US-10-086-464-2 (1-647) x US-10-425-114-6300 (1-1500)  
Qy 185 GlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSer 204  
Db 11 GGAGTTCACATGGG----- 25  
Qy 205 AspHisValValThrSerLeuProProProProLysAlaProSerProProArgGlnPro 224  
Db 26 GACCATGTTGTG---AGGATGCAACAAATGAATGGTCTCTGTGGCGGAGGTGGGGT 82  
Qy 225 ProProProProProProPheMetSerSerSerGly-----GlySerAspTyrSer 242  
Db 83 GCACCAACCAACCTCTCCAAATGATGATGATGCTGAGTTAGTTAGTTCCTCAATCTAC 142

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Qy 243 AspArgProVal---LeuProProSerProGlyLeuValLeuGlyPheSerIysSer 261
Db 143 ACGGACCGGCCCTTGGCTCTCTCCCTCACCACCTTGTCTGGGCTCAAGGGGGC 202
Qy 262 ThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeu 281
Db 203 ACCTTCACTTACGAGGAATTAGCAGCTGCCACCAACGGATTCAATGATGCAAAATTGATA 262
Qy 282 GlyGlnGlyGlyPheGlyTyrValHisIysGlyValLeuProSerGlyIysGluValAla 301
Db 263 GGACAAGGTGGATTGGGTATGTCCATAAGGGTGTGTGGCTTAGTGGAAAGGAAGTGGA 322
Qy 302 ValIysGlnLeuIysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGlu 321
Db 323 GTTAAGAGCTTTAAGCAGGTAGTGGCCAGGAGAGCGAGATTCCAAAGCTGAGATTGAC 382
Qy 322 IleIleSerArgValHisIleArgHisLeuValSerLeuValGlyTyrCysIleAlaGly 341
Db 383 ATCAATTAGCGCGTCCATCGCCATCTCGTGTCACTTTGTTGGATACCTCAATTTCTGGT 442
Qy 342 AlaIysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis 361
Db 443 GGCCAGAGGATGTTGGTCTATGAATTTATTCCTCAATACACATTTGGAATATCACCTCCAT 502
Qy 362 GlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381
Db 503 GGAAAGGTTAGCCCTACCATGGATTGGCCAAGTGGGATGGGATGGCAATAGGATCCGCT 562
Qy 382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401
Db 563 AAAGGCTTGGCTTATCTTCATGAGGACTGTATCTCGTATTTATCCATCGCGATATCAAA 622
Qy 402 AlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421
Db 623 GCTGCAAAATGCTTATTGATGATAGCTTCGAAGCAAAAGTTGCTGATTTGGATTGGCT 682
Qy 422 LysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyr 441
Db 683 AGTTGACTACTGATTAATAATACTCATGTATCGACTCGTGTCTATGGGAACCTTCGGGTAC 742
Qy 442 LeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPhe 461
Db 743 CTAGCCCTCGAATATGCTCAAGTGGAAAAATGCACAGAGAGTCTGACGTTTCTCATTT 802
Qy 462 GlyValValLeuLeuLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyr 481
Db 803 GGAGTCATGCTATTGGAACCTAATACTGGGAAGCGACCTGTTGATCACACAAATGCC--- 859
Qy 482 ValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAla---SerGluGln 500
Db 860 ATGGACGACAGCTAGTACTGGCTCGACCACTTCTGACTCGTGGACTAGAGGAGGAT 919
Qy 501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnGlyTyrAspArgGluGluMet 520
Db 920 GGCAACTTTGGAGAGTGGTTGATGCAATTTTAGAGGGAAACTACGATCCTCAAGAACTG 979
Qy 521 AlaArgMetValAlaCysAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
Db 980 TCAGAAATGGCAGCTGTGCTCGCGGTAGCATTCGTCATTTGCCAAAAAAGCGTCCAAA 1039
Qy 541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
Db 1040 ATGACCCAGATTGTGAAGATATTGGAGGAGATGCTCACTGGATGACTTGAAGATGGG 1099
Qy 561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
Db 1100 ATTAAGCCGGGCAAAATGTTGCTTACAACTCTTCATCTAGCTCAGATCAGTATGACACA 1159
Qy 581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
Db 1160 ATGCAATAAATGCTGATATGCAGAAGTTTCAGAAAGGCGAGTGTCTTCTAATAGCGAGGAA 1219
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Qy 621 SerSerGlu 623
Db 1241 AGTGGTGAA 1249
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Job time : 696 secs